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, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_gss:BH370951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                     Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 538)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photornabdus luminescens W14: potential implications for virulence 20378633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photorhabdus luminescens
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ990639 538 bp DNA linear (GSS 14-AUG-
Rfc01442 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01442, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For
186 ProvalHisLysSerGlnArgThrLeuGlnSerLysSerLeu...... 199
                                                                                                                          463 TCCGGTGGGAAACGGACCGTATGAACTGAATACCTGGAATCAGACCGATT 414
                                                                                                                                                                                                233 ThrLysThrIleThrIleBisPheIleProAspAlaAsnThrAlaAlaLy 249
                                                                                                                                                                                                                                                                                                                                     249 sLeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyProProTrpGlyGluA 266
                                                                                                                                                                                                                                                                                                                                                                                                                   266 rglleProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHis 282
                                         513 ATGATITCACCGGCAGCGCTGGAAAATATGGCAAGGAGATTGGTTTTTA 464
                                                                                                                                                                     216 rplleLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGlu 232
                                                                                                                                                                                                                                                                                363 CTGGACAGCATAACTTGGCGTGCGGTGGCGGATAACAACACCCGCTCGGC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 SerPheAspValAlaGlyThrSer.....TrpLeuThrPheAs 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 nIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyrProGluHi 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 ProlleAlaSerGlyAlaPheTyrProLysAsnIleLysGlnLysGlnT
                                                                                                                                                                                                                                                                                                                                                                        313 AATGCTGCAAACCGGTGAAGCGCAGTTTGCTTTCCCC......
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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annotation of identified clones (BLASTX, BLASTN and mapping to E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles.
1 (Dases 1 to 593)
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Other_GSSS: AG-ND-119H23.TR
                                                                                                                                                                                                                                                                                     /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                      /clone="PLG01442"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 TTAGTCCGTAATAACGGCTCTGAACCGCAATCGTTAGATCCACATAAGAT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 TyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeu...LysSe 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 rAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheTleGluS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 lArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeuV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 LeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArgGlnVa 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 alGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAsp 85
                                                                                                                         Length: 89
Gaps: 3
Percent Identity: 38.202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 538
                                                                                                                                                                                                    /db_xref="taxon:29488"
                                                        Seq prime: M43 Forward
Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148.50
2.216
75.281
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244560 toactoctctacatctcggggagaactcgctattaatataagagatgaaccccgttcttt 244619

agatecaagacaagtgcgacttettteagaaateageettgteaaacatatetatgaggg

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The present sequence represents the complete genome of Chlamydia Pneumoniae, and encodes proteins AAR34584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent office media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see
                                                                                                                                                                                                         Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY34584-Y35879) can be used in immunogenic compositions as vaccines vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                sequence of the complete genome of Chlamydia pneumoniae.
                                                                                                                                                                                                                          sinusitis; purulent ofitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of Chlamydia pneumoniae
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                                                                                                    DNA; 1230025
                                                                                                                                                                                                                                                                                                                                                                                        97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                    98WO-IB01890
                                                                                                                                                                                                                                                                                                                                                                            98US-0107078
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                               Chlamydia pneumoniae.
                                                                                                AAX91990 standard;
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                                                                                                                                                     13-SEP-1999
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                                                                                                                                                                                                                                                                                                                      03-JUN-1999.
                                                                                                                                                                                Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffais R;
                                                                                                                           AAX91990;
                                                                    RESULT
AAX91990
ID AAX91
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244799
                                                                                                           244800 cgacccttaacagctgaagactttatagaatcttggaaacaagtagctactcaagaagt 244859
                                                                                                                                                                               Db 245100 toctaaaaatatcaaacaaaaaaaaatggataaaactotcaaaaaacccccactactataa 245159
                                                                                                                                                                                                                                                                                                                                                            301 attagttcaagaaaataatctttcaggaaatatagagcctgctcttgcagaagactactc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                  245400 agaagcettagcateagcettagataaggaagetettgteteaactatattettaggeeg 245459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acacetetecatagaceattttggagtgeactetectaatgaatetaeaettgttgttae 600
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                                                               tettteeteggaeggaeteaettataeatttaaaetgaaateagetttttggagtaatgg
                                                                                                cgaccccttaacagctgaagactttatagaatcttggaaacaagtagctactcaagaagt
                                                                                                                                                                                                          cctggaatccccaacctcgcatttcttaaaacttttagctcttccagtctttttccccgt
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1 acttcccccctgctaaactatgctcagataatgctgctatgattgcaggtctaggggag 60

1; Gaps

1; Indels

DB 20; Length 1230025;

Score 1786.4; Pred. No. 0; Pred. No. 0; 0; Mismatches

99.38;

Similarity

Best Local Sim Matches 1798; Query Match

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Conservative

61 aaaattttoaaaaaaactctagtattooggaaattogtatatgogcaagatatcagtggg 120

aatotgtatoaccattotocttagcototccgtagtoctccaaggctgcaaggagtccag

121

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181

teactectetaeatetogggggggagaetegetattaatataagagatgaaccccgttett 240

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245820 ctttgcttatccatcaggagttcctccttatgcaatcaaccataaggacttcctagaaat 245879
                                                                                                                                                                                                                             Db 246060 gttatgctaaggaaaattagcacctcttttaatctcgcaaacttgtcaagaactgaatct 246119
                                                                     ctctttagctacaggaggatggttcgcagactttgctgatcctatggcatttctaacgat 1440
                                                                                                                                       1441 ctttgcttatccatcaggagttcctccttatgcaatcaaccataaggacttcctagaaat 1500
                                                                                                                                                                                                                                                                             1561 ttctctttacctagagacctttcatatttgagccgatctaccacgacgcatttcaatt 1620
                                                                                                                                                                                                                                                                                                                                               1621 tgctatgaataaaaaactttc-taatctaggagtctcaccaacaggagttgtggacttcc 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oy 1740 tatactaaactgggtgcctttgtggcacctcgtttccttctgactgctttctctcta 1799
1321 tatccctattgtcggaaaggaatttgctcttctccaagcagacctatcttcagggaactt 1380
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Complete genome sequence of Chlamydia trachomatis.
AAZ01425/c
ID AAZ01425 standard; DNA; 1038602
               (first entry)
               07-0CT-1999
         AAZ01425;
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Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymilis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

Chlamydia trachomatis

W09928475-A2

10-JUN-1999

98US-0107077 04-NOV-1998;

98WO-IB01939

27-NOV-1998;

97FR-0015041. 97FR-0016034. 17-DEC-1997; 28-NOV-1997

(GEST) GENSET

Griffais R;

WPI; 1999-371125/31

Senome sequence of Chlamydia trachomatis

Claim 1; Page 373-656; 1755pp; English

The present sequence represents the complete genome of Chlamydia trachomatis. Open reading frames (ORFs) of the genome encode

ġ polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and tihozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendeminc trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perhepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneral lamphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases. Db 252200 ACTTCCTTCTTCGCAGTTATGTTCAGACACGCTGCAATGATAGCTGGGTTAGGAGAGA 252141 ------CGTGAATAAGGATTCTGGATTTTTTGCCAAAGATGATCATCATCTTGTTAT 251634 251573 PGFGCATTCGCAGCATCAGATATGGAAAGAAGAAAAATCTTCTTCCGATATCTACTGGAGC 251514 251513 TTTTTTCTTAAAAGAGAAGAAGACCGAAGATGGTTAAAGCTAGAGAAGAGCCCTTACTA 251454 251453 CTATAATAAAGACCAGGTAGCTGTACAGGAGATCTGTATACACATCCTTGTTCATCAACA 251394 Db 252140 GACTGTTTTGCAATCGCACACATGTTTCTAAGGAGGTCATTCCATGCGCAAGATATCAGT 252081 251900 AGGATTGGTACAAGAA---ACTCCTTCTGGAGAAGTCTTCCCTGCTTTAGCGGAGAGTTT 251844 251633 CAATCTCCTCACTCCAACTCCACATTTTCTAAAGCTGCCTTACCCTCCCCGTATTTTATCC 251574 252080 GGGAATCTGCTTGCTCCTAGCATTAGCAACTTCTGGATGTTCAAAATCCTCCTCTAACGC 252021 252020 AACCCATCGGTCTCCAGCTACTCACAGTTGCTGTAAGCGTAAAAGATGATCCTGGCAC 251961 251960 ATTIGATCCTCGAGAGGTTCGCCTTCTTTCTGATATCAATTTGATTCATCATCTTATGA 251901 Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432 other; 774 aaaattttcaaaaaaactctagtattcc---ggaaattcgtatatgcgcaagatatcagt 117 gggattagttcaagaaaataatctttcaggaaatatagagcctgctcttgcagaagacta 357 358 ctctctttcctcggacggactcacttatacttttaaactgaaatcagctttttggagtaa 417 478 agteteaggaatetatgettttgeettgaateeaattaaaaatgtaegaaagateeaaga 537 gggacacctctccatagaccattttggagtgcactctcctaatgaatctacattgttgt 597 tttagatccaagacaagtgcgacttctttcagaaatcagccttgtcaaacatatctatga 297 tggcgaccccttaacagctgaagactttatagaatcttggaaacaagtagctactcaaga 477 gggaatctgtatcaccattctccttagcctctccgtagtcctccaaggctgcaaggagtc 177 1 acttocccctgctaaactatgctcagataatgctgctgctatgattgcaggtctaggggggg 60 taccctggaatccccaacctcgcatttcttaaaacttttagctcttccagtcttttccc cgttcat---aaatctcaaagaaccctgcaatccaaatcttacctatagcaagcggagc tttotatcotaaaaatatoaaacaaaaacaatggataaaactotoaaaaaaccotoacta ctataatcaaagtcaggtggaaactaaaacgattacgattcacttcattcccgatgcaaa Length 1038602; cagteactectetaeatetegggggggggagactegetattaatataagagatgaaceeegtte 50; Indels DB 20; e-115; Score 449.6; DB 20; Pred. No. 2.4e-115; 0; Mismatches 696; 251723 IGICGCTAGTATTATTCTTTCCCCTATTGA-25.0%; 56.7%; 976; Conservative Similarity Query Match Best Local S 178 715 238 298 418 538 775 251843 598 658 Matches 251684 g g qq g qq g 엄 g ΩD g g δŽ δŽ QΛ ö ğ ŏλ δ δ à ŏ δğ 88888888888888 ŏ ð

to: 1799 from: 1 to: AAD20238 Align seg 1/1

| 1 MetArglyslleSerVal6lylleCyslleThrIleLeuleuSerleuse 17 | | _ |
|--|--|--|
| 1 MetArglysileSerValGlyIleCysileThrIleLeuleuSerLeuSe | 17 | 150 |
| 101 | MetArglysileSerValGlyIleCysIleThrIleLeuLeuSerLeuSe | ATGCGCAAGATATCAGTGGGAATCTGTATCACCATTCTCCTTAGCCTCTC |
| | _ | 101 |

- 34 17 rValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgG
- 50 34 lyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArg
- 67 GlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGl 201 51
 - 300 CAAGTGCGACTTCTTTCAGAAATCAGCCTTGTCAAACATATCTATGAGGG
- 350 84 yLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaG 63 301
- 100 luAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLys 84
- 117 101
- SerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGl 401
- uSerTrpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheA 134 ATCTTGGAAACAAGTAGCTACTCAAGAAGTCTCAGGAATCTATGCTTTTG 117 451
- 134 laLeuAsnProIleLysAsnValArgLysIleGlnGluGlyHisLeuSer 150
- 501
- 151 IleAspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh 167 551
- CCIGGAAICCCCAACCICGCAITICITAAAACTITIAGCICTICCAGIC 650 rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP 184 167 601
- TITICCCCGTTCATAAATCTCAAAGAACCCTGCAATCCAAATCTCTACCT 700 hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro 200 184 159
- IlealaSerGlyAlaPheTyrProLysAsnIleLysGlnLysGlnTrpIl 201
- 234 ysThrIleThrIleHisPheIleProAspAlaAsnThrAlaAlaLysLeu
- 251 PheasnGlnGlyLysLeuasnTrpGlnGlyProProTrpGlyGluargIl 267
- 267 eProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerP
- heaspvalalaGlyThrSerTrpLeuThrPheasnIleasnLysPhePro 300 284

| ō | 51 IIGAIGICGCAGGAACCICAIGGCICACCIICAAIAICAAIAAAIICCCC | 1000 | |
|----|--|------|--|
| Ē | 01 LeuAsn | 317 | |
| 10 | 01 CTCAACATATGAAGCTTAGAGAAGCCTTAGCATCAGCCTTAGATAAGGA | 1050 | |
| m | 17 uAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisL | 334 | |
| 10 | 51 AGCTCTTGTCTCAACTATATTCTTAGGCCGTGCAAAAACTGCCGATCATC | 1100 | |
| 'n | 34 euLeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMet | 350 | |
| 11 | 01 TCCTACCTACAAATATTCATAGCTATCCGAACATCAAAAACAAGATG | 1150 | |
| m | 51 AlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGl | 367 | |
| 11 | 51 GCACAACGCCAAGCTTACGCTAAAAAACTCTTTAAAAAGCTTTAGAAG | 1200 | |
| m | 67 uLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProV | 384 | |
| 12 | 01 ACTCCAAATCACTGCTAAAGATCTCGAACATCTTAATCTTATCTTTCC | 1250 | |
| ĸ | 84 alSerSerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTr | 400 | |
| 12 | 51 TITCCTCGTCAGCAAGTICTTTACTAGTCCAACTTATACGAGAACAGTGG | 1300 | |
| 4 | 01 | 417 | |
| 13 | 01 AAAGAAAGTTTAGGGTTCGCTATCCCTATTGTGGAAAGGAATTTGCT | 1350 | |
| 4 | 17 uLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyT | 434 | |
| 13 | 51 TCTCCAAGCAGACCTATCTTCAGGGAACTTCTCTTTAGCTACAGGAGGA | 1400 | |
| 4 | 34 rpPhealaAspPhealaAspProMetalaPheLeuThrIlePhealaTyr | 450 | |
| 14 | 01 GGTTCGCAGACTTTGCTGATCCTATGGCATTTCTAACGATCTTTGCTTA | 1450 | |
| 4 | 51 ProSerGlyValProProTyrAlaileAsnHisLysAspPheLeuGluIl | 467 | |
| 14 | 51 CCA | 1500 | |
| 4 | 29 | 484 | |
| 15 | 01 TCTACAAAACATAGAACAAGAGCAAGATCACCAAAAACGCTCGGAATTAG | 1550 | |
| 4 | 84 | 200 | |
| 15 | 51 TGTCGCAAGCTTCTCTTTACCTAGAGACCTTTCATATTATTGAGCCGAA | 1600 | |
| w | 501 TyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAsnLeuGl | 517 | |
| , | 11111111111111111111111111111111111111 | 1650 | |

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss. Nucleotide sequence of the complete genome of Chlamydia pneumoniae seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX91990 1651 AGTCTCACCAACAGGAGTTGTGGACTTCCGTTATGCTAAGGAAAAT 1696 517 yValSerProThrGlyValValAspPheArgTyrAlaLysGluAsn 532 1230025 (first entry)

m Page

Genome sequence of Chlamydia pneumoniae Claim 1; Page 291-611; 1912pp; English. Chlamydia pneumoniae. WPI; 1999-357842/30 GEST) GENSET 20-NOV-1998; WO9927105-A2 21-NOV-1997; 04-NOV-1998; 03-JUN-1999 Griffais R;

98US-0107078 97FR-0014673 98WO-IB01890

The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34884-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, encoded by the open reading frames of the C. pneumoniae genome (see AAX34584-Y3579) can be used in immunospenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.

Sequence 1230025 BP; 367213 Å; 249833 C; 249013 G; 363589 T; 377 other;

Gaps: 1 Percent Identity: 99.812 Length: Quality: 2726.00 Ratio: 5.124 Percent Similarity: 99.812 US-09-824-567-2 x AAX91990 alignment_scores: alignment_block

to: 1230025 from: 1 to: AAX91990 Align seg 1/1

50 34 lyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArg

34

2 GlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGl 51

244629

67 yLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaG

84 luaspTyrSerLeuSerSeraspGlyLeuThrTyrThrPheLysLeuLys 100

SerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGl 101

245029 184 217 250 laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer 167 rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP 151 IleAspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh 184 hePheProvalHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro 245030 TITICCCGTICATAAATCICAAAGAACCCTGCAATCCAAATCICTACCT IleAlaSerGlyAlaPheTyrProLysAsnIleLysGlnLysGlnTrpIl eLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrL ysThrIleThrIleHisPheIleProAspAlaAsnThrAlaAlaLysLeu 134 217 201 234

245279 267 PheAsnGlnGlyLysLeuAsnTrpGlnGlyProProTrpGlyGluArg11

245229

284 eProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerP

245429 uAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisL

LeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGl

301

317

euLeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMet 334

351 AlaGlnArgGlnAlaTyrAlaLysLvsLeuPheLysGluAlaLeuGluGl

245629 uLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProV 384 alSerSerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrp 367

401 LysGluSerLeuGlyPheAlaIleProIleValGlyLysGluPheAlaLe

417 uLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyT 434

us-09-824-567-2.rng

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trachomatis. Open reading frames (ORFs) of the genome encode polypeptides AAX36754-Y37949. The polypeptides can be used as vaccines against chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
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                                                                                                                                                                                                                                                       245830 CCATCAGGAGTICCTICCTIATICCAATCAACCATAAGGACTICCTAGAAAT 245879
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                             245730 TCTCCAAGCAGACCTATCTTCAGGGAACTTCTCTTTAGCTACAGGAGGAT 245779
                                                                                                                                                                                                                                                                                                                                                                                  245880 TCTACAAAACATAGAACAAGAGCAAGATCACCAAAAACGCTCGGAATTAG 245929
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                                                                                       434 rpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr 450
                                                                                                                                                                                                                      451 ProSerGlyValProProTyrAlalleAsnHisLysAspPheLeuGluIl 467
                                                                                                                                                                                                                                                                                                                                           eLeuGlnAsnIleGluGlnGlnGlnAspHisGlnLysArgSerGluLeuV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 alSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIleGluProIle 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 lyValSerProThrGlyValValAspPheArgTyrAlaLysGluAsn 532
                                                                                                                           245780 GGTTCGCAGACTTGCCTGATGCCATTTCTAACGATCTTGCTTAT
Complete genome sequence of Chlamydia trachomatis.
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ID AAZ01425 standard; DNA; 1038602 BP.
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97FR-0015041.
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28-NOV-1997;
17-DEC-1997;
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use in
                                                                                                                           Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432 other;
epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251592 CCCTCCCCGTATTTATCCTGTGCAT...TCGCAGCATCAGATATGGAAA 251546
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                                                                                                                                                                                                                                   Length: 539
Gaps: 10
Percent Identity: 50.278
                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AAZ01425 from: 1
                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-824-567-2 x AAZ01425/rev
                                                                                                                                                                                                                                                                 Ratio: 3.146
Percent Similarity: 79.963
                                                                               treating these diseases
                                                                                                                                                                                                                                         Quality: 1356.00
                                                                                                                                                                                                                      alignment_scores:
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/dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
t 111 c 129 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS BH370951 593 bp DNA linear GSS 10-DEC-2001
DEFINITION AG-ND-119H23.TF ND-TAM Anopheles gambiae genomic clone AG-ND-119H23
annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles.

(bases 1 to 593)
Shetty, J., Mallek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Other_GSSs: AG-ND-119H23.TR
                                                                                                                                                                                                                                                    /clone_lib="Photorhabdus luminescens strain W14 M13 library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 TIAGTCCGTAATAACGCCTCTGAACCGCAATCGTTAGATCCACATAAGAT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 TGAAGGAGTGCCACAATTAGCCCCGTGATCTGTTTGAAGGTGTTG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 TCAICGITGGCCCG...AATGGCGAAATITTGCCAGGTTCTGCGACCAGT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 TGGGAA...AATAAAGACTTTACCGTCTGGACATTCCATATGCGTAAAGA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 rAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGluS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeu...LysSe 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 LeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArgGlnVa 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAsp 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 lArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeuV
                                                                                                                                           1. .538 /
/organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 38.202 Percent Identity: 38.202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: AQ990639 from: 1 to: 538
                                                                                                                                                                                                                    /db_xref="taxon:29488"
/clone="PLG01442"
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        African malaria mosquito.
                                                                        Seq primer: M13 Forward
                                                                                                                                                                                                /strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH370951.1 GI:17317076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 erTrpLysGlnValAla 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 GTTGGCAACGTCTGGCC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.216
75.281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148.50
                                                                                                 Class: shotgun.
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BH370951
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LOCUS BH370951
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
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JOURNAL
COMMENT
                                                                                                                     FEATURES
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ffrench-Constant, N. Materfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appli. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A0990639 14-AUG
Rfc01442 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01442, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is one of 2,122 random reads from the M13 library. For
186 ProValHisLysSerGlnArgThrLeuGlnSerLysSerLeu...... 199
                                                                                            200 .ProlleAlaSerGlyAlaPheTyrProLysAsnIleLysGlnLysGlnT 216
                                            513 ATGATTTCACCGGCAGCGCTGGAAAATATGGCAAGGAGATTGGTTTTA 464
                                                                                                                                         463 TCCGGTGGGAAACGGACCGTATGAACTGAATACCTGGAATCAGACCGATT 414
                                                                                                                                                                                        216 rplleLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGlu 232
                                                                                                                                                                                                                                                                                     233 ThrLysThrlleThrlleHisPhelleProAspAlaAsnThrAlaAlaLy 249
                                                                                                                                                                                                                                                                                                                     363 CTGGACAGCATAACTTGGCGTCCGGTGGCGGATAACAACACCGCTCGGC 314
                                                                                                                                                                                                                                                                                                                                                                               249 sLeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyProProTrpGlyGluA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 TIGTGAAGGTGAAAAATTCGCGGGTTACTGTCAGCCAGGATTGCCCAAA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 rglleProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHis 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 SerPheAspValAlaGlyThrSer.....TrpLeuThrPheAs 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 TTG.....ATGGGCCAGTCAATTATGCAGGGTTATATCAGTATGAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 erAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyArgAla 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 LysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyrProGluHi 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 ACGCCATTAACCGTCCGGCGCTGGTGAAGTTGCCTTTGCGGGCTATGCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ACGCCAGCTACTGGTGTGGTACCGCCAAGTAI...GCCTACGCGCAAAG 38
                                                                                                                                                                                                                                                                                                                                                                                                                            313 AATGCTGCAAACCGGTGAAGCGCAGTTTGCTTTCCCC.
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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Photorhabdus luminescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ990639
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Percent Similarity:
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COMMENT
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KEYWORDS
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                                                                                                                                          This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of bar from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 TrpLeuThrPheAsnIle.AsnLysPheProLeuAsnAsnMetLysLeuA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 rgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLeuValSerThrIle 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 PheLeuGlyArgAlaLysThrAlaAspHisLeuLeuProThrAsnIleHi 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476 Trcaaagacagcgcacgccgsccrarrcgaracreccgcggcargcr 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 sSerTyrProGluHisGlnLysGlnGluMetAlaGlnArgGlnAlaTyrA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 GGGCTATAACGAC...AAACTGCCCGAATACGCTTACAACCCGGAAAAAG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 laLysLysLeuPheLysGluAla...LeuGluGluLeuGlnIleThrAla 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 LysAspLeuGluHisLeuAsnLeuIlePheProValSerSerAlaSe 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 rSerLeuLeuValGlnLeuIleArgGluGlnTrpLysGluSerLeuGlyP 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 healalleProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeu 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TAAAAGCCAAAATCGTCACCTGGGAATGGGGCCAGTATCTGGCCGGGTTG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 SerSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAl 439
             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="AG-ND-119H23"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
180 c 171 g 145 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 6
Percent Identity: 29.560
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: BH370951
Contact: Brendan J Loftus
                                                                                                                          Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="PEST"
                                                                                                                                                                                                                                                                                                                           partial digest.
Seq primer: M13 For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-567-2 x BH370951/rev
                                                                               Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.384 62.264
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                                                                                                                                                                                                                                                                                                                                                                    Class: BAC ends.
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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ORIGIN
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Another Vector: play217; Genomic DNA from Rhodobacter Sphaeroides was prepared and partially digested with Sau3A1. Size selected (20kb) fragments were subcloned into the BglII site of the cosmid vector play2917 (Allen, L. N. and R. S. Hanson. 1985. Journal of Bacteriology. 161:955-962. The library was then ordered around chromosome II of Rhodobacter sphaeroides (Choudhary et al., 1994. Journal of Bacteriology, 176:764-7702). The cosmids were then digested with a variety of restriction enzymes (BamHI, EcoRI, BgIII, PStI, EcoRV, NotI and
                                                                                                                                                                                                                                                                                             GSS 15-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodobacter.

1 (bases 1 to 601)

Choudhary, M., Mackenzle, C., Nereng, K., Sodergren, E., Weinstock, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNasel) and restriction fragments subcloned into the respective multiple cloning site sites of pBluescript SK (-). Note BglII fragments were subcloned into the PBluescript BamHI site. DNaseI fragments were subcloned into the Ecosy Site. All subclones were transformed into the sequences where passible were assembled using the contract of the sequences where possible were assembled using the
                                                                                                                                                                                                                                                                                    B07758 601 bp DNA linear GSS 15-NOV-199 8219PIOIED1120195T7 Rhodobacter sphaeroides 2.4.1 genomic DNA library Rhodobacter sphaeroides genomic clone 8219PIOIE01120195T7 similar to dppA (P23847), DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="8219F101E01120195T7"
/clone_lib="Rhodobacter sphaeroides 2.4.1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Kaplan, S.
Low-resolution sequencing of Rhodobacter sphaeroides 2.4.1T;
| 191 CGCAAAGGGGAACAGCAGGCGCGCTGTATGGCTGGATGTCGGATAACGG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mackenzie, C.
Department of Microbiology and Molecular Genetics
The University of Texas Health Science Center
6431 Fannin St., Houston, TX 77006, USA
Tel: (713) 794-1742
Fax: (713) 794-1782
Email: mackenz@utumg.med.uth.tmc.edu
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Percent Identity: 28.125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome II is a true chromosome
Microbiology 143, 3085-3099 (1997)
98015398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: pBluescript SK (-) T7 Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="2.4.1T"
/db_xref="taxon:1063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                     439 aAspProMetAlaPheLeuThrile 447
                                                                                                                            141 CGACCGGACACTTCGCTACCCTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter sphaeroides. Rhodobacter sphaeroides
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B07758.1 GI:2055550
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1.415
55.000
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LOCUS B07758
                                                                                                                                                                                            seq_name: gb_gss:B07758
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alignment_block:

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/dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."
139 c 130 g 187 t 5 others
  annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
Seg primer: M13 Forward
Class: shotgun.
                                                                                                                                                                                                                                    /clone="PLGG1703"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 sPhelleProAspAlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLysL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 euAsnTrpGlnGlyProProTrpGlyGluArgIleProGlnGluThrLeu 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 ......TGTATC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 SerAsnLeuGlnSerLysGlyHisLeuHisSerPheAspValAlaGlyTh 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCAGTCCTTACCTTTGTACGTTTTATTACGAAATTACCAATAAAAACCC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..........AsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAsp 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 GCCGTTTACTTGATGTCAGAGTCCGCGAAGCCGTCAAGTTAAGTCTCGAT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 LysGluAlaLeuValSerThrIlePheLeuGlyArgAlaLys...... 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 ......ThralaaspHisLeuLeuProThrAsnIleHisSerTyrProG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 TATGGTTTTACGCCAACATTTATCGGGTGGCGGCGATTTTGTTAAGCCAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 luHisGlnLysGlnGluMetAlaGlnArgClnAlaTyrAlaLysLysLeu 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 PheLysGluAla......LeuGluGluLeuGlnIleThrAlaLy 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: :::111
252 TTAGCTCAGGCCGGTTTCAATCAGGCGAATCCATTGAAGTTCACA.... 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 sAspLeuGluHisLeuAsnLeuIlePheProValSerSerSerAlaSerS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 rSerTrpLeuThrPhe.....AsnIleAsnLysPheProLeuAsn....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 ProHisTyrTyrAsnGlnSerGlnValGluThrLysThrIleThrIleHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 AGAAAATNAAGAAAGAGA.....TICNIGAICAGGIICGC
                                                                                                                                                                       luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 21.992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                     1. .613
/organism="Photorhabdus lu/
/strain="R14"
/db_xref="taxon:29488"
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AQ990866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-567-2 x AQ990866/rev
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1.021
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                                                                                                                                             source
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                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A0990866 613 bp DNA linear GSS 14-AUG-2000 Rfc01703 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01703, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Photorhabdus.
1 (bases 1 to 613)
Ifrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: Dssrfc@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For
                                                                                                                         94 rTyrThrPheLysLeuLysSerAlaPhe...TrpSerAsnGlyAspProL 110
                                                                                                                                                                                                                             484 CTANACGITCAAGNIGCGCCCGGGCGIGAAAIICCACAAGGGCCGCGAGA 435
                                                                                                                                                                                                                                                                           110 euThrAlaGluAspPheIleGluSerTrpLysGlnValAlaThrGlnGlu 126
                                                                                                                                                                                                                                                                                                                       434 TGACGGCCGAGGATGTGAAATATTCGNTCGACCGCGTGACCCTGCCG 385
                                                                                                                                                                                                                                                                                                                                                                     127 ValSerGlyIleTyrAlaPheAlaLeuAsnProIleLysAsnValArgLy 143
                                                                                                                                                                                                                                                                                                                                                                                                            384 ACCCAGTCGCGGGCGAGGCTTNTTCGGCTCGATCAAGGGCTTCGATGC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 slleglnGluGlyHisLeuSerIleAspHisPheGlyValHisSerProA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 GATGGCNGACGGCTCGGCCAGCACGCTCGAG...GGCGTGACGGTGGTCG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           snGluSerThrLeuValValThrLeuGluSerProThrSerHisPheLeu 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 ATCCCTCGACCGTCAGGATCGAGCTCTNGCGTCCCGACGCCACCCTTCCTG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 LysLeuLeuAlaLeuProValPhePheProValHisLysSerGlnArgTh 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 CATGTGATGGCGNTGAANTTCGCCTCGGTGGTGCCGAAGGAAGCCGTCGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 GGCGGCGGGCGGANTTCGCCAAGCAGCGGTCGGCACCGGGGCCTTC. 139
                                                                                                        94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....AAGCTCGCCGAATGGACGCTGGGCCAGCGTCTCGTN 103
                                                                                     78 IleGluProAlaLeuAlaGluAspTyrSerLeuSerSerAspGlyLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rLeuGlnSerLysSerLeu......ProlleAlaSerGlyAlaPheT
                                                            to: 601
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Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 LeuSerLysAsnProHisTyrTyrAsnGln 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 TTCGAGAAGACGCCGACTACTGGCGCGAG 73
                                           Align seg 1/1 to reverse of: B07758
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Photorhabdus luminescens
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US-09-824-567-2 x B07758/rev
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group; Rhodobacter.
1 (bases 1 to 713)
Choudhary, M., Mackenzie, C., Mouncey, N., Weinstock, G.M. and Kaplan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
AQ012177
DEFINITION 2711C073112697 Cosmid library of chromosome II Rhodobacter spheroides genomic clone 2711C073112697, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lip="Cosmid library of chromosome II"
/lab_host="E. coli S17-1"
/note="Vector: plA2917"
a 250 c 216 g 115 t
                     236 eThrileHisPhelleProAspAlaAsnThrAlaAlaLysLeuPheAsnG 253
                                                   253 lnGlyLysLeuAsn.....TrpGlnGly.....ProPro 262
                                                                                                                                                                                                  263 TrpGlyGluArgIleProGlnGluThrLeuSerAsnLeuGlnSerLysGl 279
                                                                                                                                                                                                                                                               ......AATGG 180
                                                                                                                                                                                                                                                                                           279 yHisLeu.....HisSerPhe.AspValAlaGlyThrSerTrpLeuThr 293
                                                                                                                                                                                                                                                                                                                     294 PheasnileasnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLe 310
                                                                                                                                                      105 CTGGGGAAAATAGACCTGATCTATGGAACGGAAGGGCCGATTTCCCCCGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                310 uAlaSerAlaLeuAspLysGluAlaLeuValSerThrilePheLeuGlyA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RsGDB, the Rhodobacter sphaeroides Genome Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
Contact: Choudhary, M.
Department of Microbiology and Molecular Genetics
University of Texas Medical School
6431 fanin Street, Houston, TX 77030, USA
Tel: 713 500 5439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rhodobacter sphaeroides"
/strain="2.4.1r"
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Gaps: 5
Percent Identity; 23.256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 rgAlaLysThrAlaAspHisLeuLeuProThrAsnIle 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 CACAGAAGCGTGCAGATACCCTGTTTGCCGATAATGTT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: madhu@utmmg.med.uth.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:1063"
/clone="2711C073112697"
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                                                                                                                                                                                                                                               155 TACTITCGAGCGCTICCAGAA.....
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Rhodobacter sphaeroides
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1.180
56.395
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AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                          A2302752 402 bp DNA linear GSS 06-MAR-2001 GSSBrul690 Brucella abortus random genomic library Brucella melitensis biovar Abortus genomic clone UU1690, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 402)
Sanchez, D.O., Zandomeni, R.O., Cravero, S., Verdun, R.E., Pierrou, E.,
Faccio, P., Diaz, G., Lanzavecchia, S., Aguero, F., Frasch, A.C.C.,
Andersson, S.G.E., Rosetti, O.L., Grau, O. and Ugalde, R.A.
Gene discovery through genomic sequencing of Brucella abortus
Infect. Immun. 69 (2), 865-868 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Siv.Andersson@ebc.uu.se
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brucella melitensis biovar Abortus.
Brucella melitensis biovar Abortus
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UD1690"
/clone_lib="Brucella abortus random genomic library"
/note="Vector: modified M13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Brucella melitensis biovar Abortus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Small Genomes Sequencing Group
Department of Molecular Evolution, Uppsala University
Norbyvaen 18C, 5752 36, Uppsala, Sweden
Tel: 46-18-471-4379
390 erLeuLeuValGlnLeuIleArgGluGlnTrpLysGluSerLeuGlyPhe 406
                                     176 AGCAGGCTATC...GCCGCCGCATGTGGGAAAAGAATTGGGAGCG 130
                                                                                                                                                                           423 rSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaA 440
                                                                                                                              129 GATGTGATTTTACAGAATCAGGAATGGAAAACCTCTCTTGAAAGCCGCCA 80
                                                                                                                                                                                                              79 TCAAGGGAATTATGAGGTGACCAGAGCAACCTGGTGTGCTGATTACAATG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 SerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrLysThrll 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407 AlalleProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 27.692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="2308"
/db_xref="taxon:235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                      440 spProMetAlaPheLeuThrIle 447
                                                                                                                                                                                                                                                                                                AZ302752.1 GI:10128963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Siv Andersson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 46-18-471-6404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouality: 118.00
Ratio: 1.595
milarity: 56.923
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US-09-824-567-2 x AZ302752
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Source

FEATURES

BASE COUNT

ORIGIN

LOCUS DEFINITION

ACCESSION

SOURCE ORGANISM

KEYWORDS

VERSION

REFERENCE AUTHORS JOURNAL

TITLE COMMENT

GSS 04-JUN-1998

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/tissue_type="membry"
/dev_stage="2-cell"
/lab_host="npH10B"
/note="organ: embryo; Vector: pBluescribe (modified);
Site_1: Mlu1; Site_2: Sal1; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Priner: Sal1(dT): 5'-CGGTGGCGTGTGTGTTTTTTTTTTTTT-3'.
were cloned into the Mlu1/Sal1 sites of a modified pBluescribe vector using commercial linkers (NEB).

Average insert size: 1.2 kb."
69 a 129 c 126 g 66 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 02-JUN-1999
                                                                                                                                                                                   This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Possible reversed clone: similarity on wrong strand
Seq primer: Primer name ambiguous
High quality sequence stop: 373.

Location/Qualifiers
                        4444 Forest Park Parkay, Box 8501, St. Louis, MO 63108, USA Tal: 314 286 1800
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:949302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nbxb0096M13f CUGI Rice BAC Library Oryza sativa genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 ACAGCTIGCCGAGGCCAGCAGTCCTACATCTGGGCGTCGATCTTTGACA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 GluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLy 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 GAGAGCTGGAAGTACTCGGACGATCTGCGCACCTTACACTCAAGCTTCG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 GlyGluLeuAlalleAsnIleArgAspGluProArgSerLeuAspProAr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 gGlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 lyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAla 83
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:960510"
/clone_lib="knowles Solter mouse 2 cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 sSerAlaPhe...TrpSerAsnGlyAspProLeuThrAlaGlu 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 81
Gaps: 2
Percent Identity: 34.568
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  Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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AQ579158.1 GI:4979571
GSS.
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1.946
69.136
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US-09-824-567-2 x AI503668
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Ratio:
Percent Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1to 390)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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WA75604.XI Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:960510 3' similar to TR:P71370 P71370 OLIGOPEPTIDE BINDING PROTEIN; mRNA sequence.
                                                                                                              241 IleProAspAlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLys..... 255
                                                                                                                                                                                                          256 ......LeuAsnTrpGlnGlyProProTrpGlyGluArgIleP 268
                                                                                                                                                                                                                                                   63 TGTGATCGAGGATGTCGACATCCGCAACGTCCCCTGATCGAGCGCAATC 112
                                                                                                                                                                                                                                                                                                                                  roGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerPhe 284
                                                                                                                                                                                                                                                                                                                                                                                                285 AspValAlaGlyThrSerTrpLeuThrPheAsnIleAsnLysPheProLe 301
                                                                                                                                                                                                                                                                                                                                                                                                                                               GACATG.....AACTGCCAAACGGCGCCCTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 uAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 laLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAsp..... 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 ......HisLeuLeuProThrAsnIleHisSerTyrProGluHisGl 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 CCGGTGGCGCGCATCATGCCCTTCTGGGCCGAAAGGCCGCCCGAGCACCG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 nLysGlnGluMetAlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 CTACGATCCCGAGGCCGCGCGCGCTTCTGGCCGGGGCCGGGATCAAAG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 luAlaLeuGluGluLeuGlnIleThrAlaLySAspLeuGlu..... 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 GAAACGGGGGTCCTTTTCCGCGAACATGCCGCCAAGGCCGGCATCACGAT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                            from: 1 to: 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI503668
AI503668.1 GI:4401519
                                                                    Align seg 1/1 to: AQ012177
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                        US-09-824-567-2 x AQ012177
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alignment_block:
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ub_bost="axon:4530"
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/clone="lbx"cugi Rice BAC Library"
/clone=lbx"cugi Rice BAC Library"
/lab_bost="E. coil DH10B"
/note="Vector: pBelcBAC11; Site_1: HindIII; Site_2:
HindIII: Rice is one of two most popular grains in the
World. Half of the World population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Orycas activa, Nipponbare variety. The
cof 128:5 Kb providing 10:9 happioid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99:9%. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the Whole library for colony screening."
                                             Entaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Entartoideae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Ming, R.A. and Dean, R.A. A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)

Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 rcGGCCGrGCrGCCGCCrGrACCCTGCCCGCCTGGGCGGTGACG.... 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ......CICAAIAICTCGCTGGACGCGGACCCCGGCAAGCTCGACCCCA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 CGCAGTCCTCCATGCTCAACGAGCATCGTCTACCAGAGCATCTTCGAC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 gGlyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 SerValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerAr 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 rgGlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGlu 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 5
Percent Identity: 27.536
                                                                                                                                                                                                                                                                                  Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 303.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                  Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.276
61.594
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                             Oryza sativa
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                          ORGANISM
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                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                           AUTHORS
                                                                                                                              REFERENCE
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SOURCE
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1 (bases 1 to 498)
Choudhary,M., Mackenzie,C., Nereng,K., Sodergren,E., Weinstock,G.M.
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16:1955-962. The library was then ordered around
chromosome II of Rhodbacter sphaeroides (Choudhary et
al., 1994. Journal of Bacteriology, 176:7694-7702). The
cosmids were then digested with a variety of restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8025R101A0708289573 Rhodobacter sphaeroides 2.4.1 genomic DNA library Rhodobacter sphaeroides genomic clone 8025R101A0708289573 similar to dppA (F23847), DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pLA2917; Genomic DNA from Rhodobacter
sphaeroides was prepared and partially digested with
Sau3AI. Size selected (20kb) fragments were subcloned i
the BgIII site of the cosmid vector pLA2917 (Allen, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter sphaeroides
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Rhodobacter sphaeroides 2.4.1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Low-resolution sequencing of Rhodobacter sphaeroides 2.4.1T:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mackenzie, C.
Department of Microbiology and Molecular Genetics
The University of Texas Health Science Center
6431 Fannin St., Houston, TX 77006, USA
Tel: (713) 794-1742
Fans: (713) 794-1782
Fans: (713) 794-1782
Fans: paluescript SK (-) T3
Class: shotgun.
                                         100 ..LysSerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPhe 115
                                                                                                                                                                                                                                                                                                                     116 IleGluSerTrpLysGln...ValAlaThrGlnGluValSerGlyIleTy 131
                                                                                                                                                                                                                                                                                                                                                        503 ...AGGCGGTGGAATTCACCTGTTGGCGGCAAGAGAGACCTCCTTGCG 549
                                                                                                                                                                                                                                                                                                                                                                                                                           131 rAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGlnGluGlyH 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAl
                                                                                                                                                                                                                                                83 aGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .498
/organism="Rhodobacter sphaeroides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome II is a true chromosome
Microbiology 143, 3085-3099 (1997)
98015398
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/db_xref="taxon:1063"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 isLeuSerIleAsp 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_gss:B07745
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genome sequencing Genome Campus, Hinxton,

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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melvilles, S.E., Rajandream, M.A. and Barrell, B.G. Direct Submission
Submisted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hill Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 LeuPheAsnGlnGly...LysLeuAsnTrpGlnGlyProProTrpGlyGl 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AAGGGTACCGCAGGTTTCGACGACGATGGAGGAGCTCGCCAGCACCAGCA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 AlaGlyThrSerTrpLeuThrPheAsnIleAsnLysPheProLeuAsnAs 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 alSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisLeuLeuPro 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 AAAACACTGTCATATGCGGACAAGCGCGTGAAATTGAGCGTTTGCG... 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 ThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMetAlaGlnAr 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 ......CGTGAGGTTGAAGAACTTCGCGGCACACTTGTCTCTCA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 gGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGlnI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 luThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerPheAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 nMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 4
Percent Identity: 24.476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 TCAGGGCCATTCTCAGACCTTTTCTCCGTG......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="380g06'
115 c 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: TA380G06P
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                     TITLE
JOURNAL
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ORIGIN
                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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                                                                                                                                                                                                    COMMENT
DNSSEI) and restriction fragments subcloned into the respective multiple cloning site sites of pBluescript SK (-). Note BBILL fragments were subcloned into the pBluescript BamHI site. DNSSEI fragments were subcloned into the ECORV site. All subclones were transformed into the sequences where possible were assembled using the GCG program GELASSEMBLE. "

a 137 c 171 g 88 t 19 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TA380G06P 519 bp DNA linear GSS 13-DEC-2000 T. brucel sheared genomic DNA clone 380g06, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 LeuThrTyrThrPheLysLeuLysSerAlaPheTrpSerAsnGlyAspPr 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 oLeuThralaGluAspPheIleGluSerTrpLysGlnValAlaThrGlnG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 luValSerGlyIleTyrAlaPheAlaLeuAsnProIleLysAsnValArg 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 sSerProAsnGluSer....ThrLeuValValThrLeuGluS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 LysileGlnGluGlyHisLeuSerIle.....AspHisPheGlyValHi 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 erProThrSerHisPheLeuLysLeuLeuAlaLeuProValPhePhePro 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 ValHisLysSer......GlnArgThrLeuGlnSerLy 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 sSerLeuProlleAlaSerGlyAlaPheTyr.ProLysAsnIleLysGln 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 CCCCTCGGCGCCCTTCCTGTCCACCATGCCGATCCCGCCGTCTCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 CIGTCGAAGGCGGCGTCGAAGCCATGGGCGAGAGGCCTATGCCGAGAA
                                                                                                                                                                                                                                                                                                                                                Gaps: 7
Percent Identity: 30.345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: B07745 from: 1 to: 498
                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 LysGlnTrpIleLysLeuSerLysAsnProHis 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 GGCGACCGAGTNATCCTAAAANANAACCCGAAT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ......GCGGCCTTCACGCTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 CATCACCNCGAGGAC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence
AL497735
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Trypanosoma brucei
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US-09-824-567-2 x B07745/rev
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56.552
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                                                                                                                                                                                                      83
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KEYWORDS
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Length:

149

to: 519

286

289

320

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LeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMetAl 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_gss:TA358F03P
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ORGANISM
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JOURNAL
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                                                                                                seq_documentation_block:
LOCUS
HH398784
DEC-2001
DEFINITION AG-ND-150B19.TR ND-TAM Anopheles gambiae genomic clone AG-ND-150B19
                                                                                                                                                                                                                                                       African malaria mosquito.
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 554)
Shetty.J., Malek.J., Koo,H., Collins.F., Gardner,M. and Loftus.B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from month patched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 uAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 laLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisLeu 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 AAGCGATTAAGCAACTTTATAAAGGTCAAGGGTTAGAGCTGAAATGTTG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftusetigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:7165"
/clone="%G-ND-150B19"
/clone_lib="ND-7AM"
/note="Vector: pECBAC1; Site_1: HindIII"
/132 c 92 g 175 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 SerTrpLeuThrPheAsn.....IleAsnLysPheProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 5
Percent Identity: 20,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other_GSSS: AG-ND-150B19.TF
Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
468 CTTCAGCAGGAAGCGCAAGGAATCAAC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to reverse of: BH398784
                                                                                                                                                                                                               BH398784.1 GI:17345000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Rev
Class: BAC ends.
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US-09-824-567-2 x BH398784/rev
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1.015
57.955
                                                                                                                                                                      , DNA sequence.
BH398784
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                                                            seq_name: gb_gss:BH398784
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Percent Similarity:
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                                                                                                                                                                                                                                                                           ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                          ACCESSION
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KEYWORDS
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GSS 13-DEC-2000
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Constructed at the Institute for Genomic DNA isolated from a cloned population of
Rockville, WD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Emails of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TA358F03P 558 bp DNA linear GSS 13-DE T. brucei sheared genomic DNA clone 358f03, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                       363
                                                                                                                                                                                                   363 luAlaLeuGluGluLeuGlnIleThrAlaLysAspLeuGluHisLeuAsn 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 eArgGluGlnTrpLysGluSerLeu......GlyPheAlalleProI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
400 GTGCCAGATGGGGTGCAAGGGCACAATGCTCAATATAGAAGTAGTGTTGC 351
                                                                                                                                                                                                                                                                                                                                              380 LeuIlePheProValSerSerAlaSerSerLeuLeuValGlnLeuIl 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 leValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSerGlyAsn 426
                                                                                                                                   350 CTATAACCCGTTATTGGCCAATAAATTACTGGATCGATTTGGTTATAAGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 PheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaAspProMetAl 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 aGlnArgGlnAlaTyrAlaLysLysLeu......PheLysG
                                                                                                                                                                                                                                                                       300 AAGGCAAAGATGGTTATCGA...ACTTTACCCAACGGGCAGCCATTTACC
                                                                                                                                                                                                                                                                                                                                                                                                208 ....GAGTTATGGAAGAAAACTTAGATGCTATTGGGGTGCGTGTTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Trypanosoma brucei"/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:5691"
/clone="358f03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 aPheLeuThrIlePheAlaTyrProSer 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TITIGCICAGIIGCITTAIGGICCGAAC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL494115.1 GI:11870744
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1 (bases 1 to 558)
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Fax: 46-18-471-6404
Email: Siv.Andersson@ebc.uu.se
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH375296 583 bp DNA linear GSS 10-DEC-2001 AG-ND-174G16.TR ND-TAM Anopheles gambiae genomic clone AG-ND-174G16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                               /clone="UU1761"
/clone_lib="Brucella abortus random genomic library"
/note="Vector: modified M13"
a 103 c 101 g 84 t
                                                                                                                                                                                                                            1. .391
/organism="Brucella melitensis biovar Abortus"
/strain="2308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 GGGTGGCGAAAATAGACCTGATCTATGGAACGGAAGGGCCGATTTCCCCC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 roTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuGlnSerLys 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 ATCAATCATGCAGTCGATAAGGACACGATGCATGCCACCGTGCTCTACGG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 GlyHisLeu.....HisSerPhe.AspValAlaGlyThrSerTrpLeuT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 hrPheAsnIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAla 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 CGCTCAACACCAATCACGCCGCAACAAAAGACCTCGCTGTCCGCAAGGCC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 LeuAlaSerAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuGl 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 ATAACTGGCAAGGTGATACCCGATCCGAATACACGGGCGATTGGCTTCGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 IleThrIleHisPheIleProAspAlaAsnThrAlaAlaLySLeuPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 nGlnGlyLysLeuAsn.....TrpGlnGly.....proP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 30,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 yArgAlaLysThrAlaAspHisLeuLeuProThrAsn 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 GACACAGAAGCGTGCAGATACCCTGTTTGCCGATAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AZ302822 from: 1 to: 391
                                                                                                                                                                                                                                                                                        /db_xref="taxon:235"
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH375296 
BH375296.1 GI:17321438
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1 (bases 1 to 583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-824-567-2 x AZ302822
                                                                                                                                                           vector.
Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
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Sanchez,D.O., Zandomeni,R.O., Cravero,S., Verdun,R.E., Pierrou,E.,
Faccio,P., Diaz,G., Lanzavecchia,S., Aguero,F., Frasch,A.C.C.,
Andersson,S.G.E., Rosetti,O.L., Grau,O. and Ugalde,R.A.
Gene discovery through genomic sequencing of Brucella abortus
Infect. Immun. 69 (2), 865-868 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melitensis biovar Abortus genomic clone UU1761, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Siv Andersson
Small Genomes Sequencing Group
Department of Molecular Evolution, Uppsala University
Norbyvagen 18C, S-752 36, Uppsala, Sweden
                                                                                                                                                                                                                                                                                                             250 LeuPheAsnGlnGly...LysLeuAsnTrpGlnGlyProProTrpGlyGl 265
                                                                                                                                                                                                                                                                                                                                           ....... G 270
                                                                                                                                                                                                                                                                                                                                                                                                                                               398 AAGGTACCGCAGGTTTCGACGACGATGGAGGAGCTCGCCAGCACCAGCA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 luThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerPheAspVal 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 GTACACTCGAGCTTCAGAGTTTCTTCGTTCTTCACACTTTGATACG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 AlaGlyThrSerTrpLeuThrPheAsnIleAsnLysPheProLeuAsnAs 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 nMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLeuV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....CTCCTCTCATGCTGCAAACATTTGGTGGATTCAAGCGTAAGTC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 alSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisLeuLeuPro 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 ThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMetAlaGlnAr 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 gGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGlnI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 GCAGAGITACTITCAGGAICTGGAGAGICGTAGAITAGCACACTCAGIGG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 TCAGGGCCATICICAGACCTITICICCGIG.....
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                                                                                                                                        1.344 Gaps: 4
53.846 Percent Identity: 24.476
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           142
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Brucella melitensis biovar Abortus
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           б
           123
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                                                                                                                                                      Percent Similarity:
      156
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Contact: Brendan J Loftus.

Contact: Brendan J Loftus.

Contact: Brendan J Loftus.

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Fax: 304 838 543

Fax: 305 843

Fax: 306 843

Fax: 307 843

Fax: 308 8
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. 
Direct Submission of BAC-end sequences from Anopheles gambiae
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 SerTrpLeuThrPheAsn......IleAsnLysPheProLe 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 laLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisLeu 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="ND-TAM"
/note="Vector: pECBACI; Site_1: HindIII"
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Gaps: 5
Percent Identity: 20.455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:7165"
/clone="AG-ND-174G16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .583
                                                                                                             Other_GSSs: AG-ND-174G16.TF
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Seq primer: M13 Rev
Class: BAC ends,
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US-09-824-567-2 x BH375296/rev
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Percent Similarity:
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ORIGIN
   AUTHORS
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- 443 aPheLeuThrllePheAlaTyrProSer 452
 - 67 TITIGGTCAGTTGCTTATGGTCCGAAC 40

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134 laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer 150
           441.50
441.00
440.50
438.50
438.50
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Ratio: 5.148
Percent Similarity: 100.000
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                                                                                                                                              seq_name: gb_pat:AX349501
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LOCUS AX349501
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           gb_ba:AF465631
gb_ba:AE002565
gb_ba:AF188935
gb_ba:ECU88242
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8 1599 | AX345501 Sequence 24 from Pate 1599 | AX263341 Sequence 1 from Pate 7 11648 | AE001606 Chlamydia pneumoniae 7 11764 | AE0012016 Chlamydophila pneumoniae 29550 | AP002216 Chlamydophila pneumoniae 11944 | AE002215 Chlamydophila pneumoniae 11947 | AE002215 Chlamydophila pneumoniae 12980 | AE002215 Chlamydophila pneumoniae 12080 | AX349505 Sequence 28 from Pater 1402 | AX300389 Sequence 28 from Pater 1402 | AE002313 Chlamydia maridarum, 1687 | AX300389 Sequence 1 from Pater 1402 | AE002313 Chlamydia trachomatic 1687 | AE002313 Chlamydia trachomatic 1687 | AE002313 Chlamydia trachomatic 1680 | AX027646 Sequence 1 from Pater 1670 | AX027646 Sequence 1 from Pater 1670 | AX027645 Sequence 1 from Pater 1670 | AX027645 Sequence 1 from Pater 1687 | AE007859 Clostridium acetobut 1587 | AA250013 Borrelia afzelii p58 6336 | AX002571 Bacillus subtilis 165553 | AX002571 Bacillus subtilis 165798 | AX36758 B.subtilis dcia operon. 1308 | AX349503 Sequence 26 from Pater 1670 | AX36758 B.subtilis dcia operon. 1308 | AX349503 Sequence 26 from Pater 1670 | AX302571 Bacillus subtilis 1670 | AX3025010 
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! AL603645 Rhizobium meliloti
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1 S75873 60 kda antigen [Borrelia
0 1 AL596173 Listeria innocua Cl
1 AF305387 Bacillus thuringiensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! AE000792 Borrelia burgdorfer
! AF103793 Listeria monocytogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ! AE008258 Agrobacterium tumef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! AE006271 Lactococcus lactis
                                                                                                                                                                  -MODEL=frame+_plan.model -DEV=xlp
-Q=/Cgn2_1/USPTO_spool/US09824567/runat_23072002_141350_13449/app_query.fasta_1.596
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-WINNATCH=0.100 -LCOPEL=0.000 -LCOPEXT=0.000 -QAPDEXT=4.000
-QGAPEXT=0.100 -LCOPEL=0.000 -LCOPEXT=0.500 -FGAPDP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FELOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FANS=humand0.cdi
-LISP=45 -DCOALIGN=200 -THR_SCORE=pct -THR_NAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LCAL -OUTFNT=pfs -NON=ext -HEAPSIZE=500
-MINLEN=0 -MAXIEN=2000000000 -USER=US09824567_@CGN1_1.7895
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                                                                                       Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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4.3e-218
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.5e-215
.3e-103
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.9e-53
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OM of: US-09-824-567-2 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query length: 532
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Database sequences: 1797656
Database length: 187333701
Search time (sec): 2484.090000
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                                             Date: Jul 26, 2002 5:53 AM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
                                                                                                                                                     Command line parameters:
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gb_pat:AX268341
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AF465631 Oenococcus oeni le
AE002565 Enterococcus faec
I AF188935 Bacillus anthraci
I U88242 Escherichia coli per
I AE000231 Escherichia coli
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                                                                                                                                                                                                                                                              Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetArgLys1leSerValGly1leCys1leThr1leLeuLeuSerLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGCGCAAGATATCAGTGGGAATCTGTATCACCATTCTCCTTAGCCTCTC
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389 c 261 q 440 t
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1886
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Ratti, G. and Grandi, G.
Immunisation against Chlamydia pneumoniae
Patent: WO 0202606-A 24 10-JAN-2002;
                                                                                                                                                             DNA
   1.6e-26
1.1e-25
3.8e-25
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                                                                                                                                                         Sequence 24 from Patent W00202606.
AX349501
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 626.24
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Murdin, A.D., Oomen, R.P., Wang, J. and Dunn, P. Chlamydia antigens and corresponding dna fragments and uses thereof Patent: Wo 0174863-A 1 11-OCT-2001; Aventis Pasteur Limited (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FWSODPLPAEDFESHKOVATOEVSGITARALINPIKNVRIIGEGELSIDHFEVENEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT 29-0CT-2001
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                                                                    1401 TCTACAAAACATAGAACAAGGCAAGATCACCAAAAACGCTCGGAATTAG 1450
                                                                                                                                                                                                                                              1501 TACCACGACGCATTCAATTIGCTATGAATAAAAACTTTCTAATCTAGG 1550
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1 (sites)
                                                                                                                                  467 eLeuGlnAsnIleGluGlnGluGlnAspHisGlnLysArgSerGluLeuV 484
                                                                                                                                                                                                                     484 alSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIleGluProIle 500
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                                                                                                                                                                                                                                                                                                          501 TyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAsnLeuGl
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101. .1699
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Gaps: 0
Percent Identity: 100.000
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1. .1799
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Percent Similarity: 100.000
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JOURNAL
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KEYWORDS
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BCT 01-DEC-2000
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Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W., Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.

Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE001606 11648 bp DNA linear BCT 01-DEC Chlamydia pneumoniae section 22 of 103 of the complete genome. AE001506 AE001363 AE001606.1 GI:4376464
1001 CTCAACAATATGAAGCTTAGAGAAGCCTTAGCATCAGCCTTAGATAAGGA 1050
                                                     Chlamydophila pneumoniae CWL029
Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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(bases 1 to 11648)

10192388 2 (bases

PUBMED REFERENCE

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GLQSELSTGGGTALGYTAALKKKQRRYILGASILQISIPAFIFATLLQYVFAVKIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSDGTPLTAYDFEKSIKQLYFEEFSPSIHTLLGVIKNSSAIHNAOKSLETLGIQAKDD
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LSKNPHYYNOSOVERTITIHFIPDANTAAKLFNOGKLNWGGPPWGERIPQETLSNLQ
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                                                                Direct Submission
Submitted (01-DEC-1998) Program in Infectious Diseases, University
of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
Location, Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1403 ATCTTGGAAACAAGTAGCTACTCAAGAAGTCTCAGGAATCTATGCTTTTG 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 SeralaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheileGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 uSerTrpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetArgLysIleSerValGlyIleCysIleThrIleLeuLeuSerLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 IleAspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 rValValLeuGlnGlyCysLysGluSerSerHisSerThrSerArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lyGluLeuAlalleAsnIleArgAspGluProArgSerLeuAspProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGl
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
                                                                                                                                                       /gene="oppF"
/note="CPn0202"
                                                                                                                                      10578. .11366
                                                                                                                                                                                              10578. .11366
/gene="oppF"
                                                                                                                    LMSMQGGL"
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Percent Similarity: 100.000
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1603 TITICCCCGITCATAARICTCAAAGAACCCTGCAATCCAAATCTTACCT 1652
                                                                                                                                                                                                                                                                  1703 AAAACTCTCAAAAACCCTCACTATATAATCAAAGTCAGGTGGAAACTA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2052
                                                                                                          553 CCTGGAATCCCCAACCTCGCATTTCTTAAAACTTTTAGCTCTTCCAGTCT 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                  2053 TCCTACCTACAATATTCATAGCTATCCCGAACATCAAAACAAGAGAGG 2102
                                                                                                                                                   hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2103 GCACAACGCCAAGCTTACGCTAAAAAACTCTTTAAAGAAGCTTTAGAAGA 2152
                                                                     rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP 184
                                                                                                                                                                                                                                                                                                                            eLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 PheasnGlnGlyLysLeuasnTrpGlnGlyProProTrpGlyGluarg11 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2203 TITCCTCGTCAGCAAGTTCTTTACTAGTCCAACTTATACGAGAACAGTGG 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGl 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 AlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 uLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProV 384
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201 IlealaSerGlyAlaPheTyrProLysAsnileLysGlnLysGlnTrpll
                                                                                                                                                                                                                                                                                                                                                                                                          ysThrIleHisPheIleProAspAlaAsnThrAlaAlaLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 rpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr
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complement(4620. .5978)
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Chlomydophila pneumoniae AR39, section 44 of 94 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:7189485"
/translation="MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEP
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FWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA On Jun 1, 2000 this sequence version replaced gi:7189484. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Read, 7.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Lihher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID:40005; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, B.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Baas, S., Linher, K., Weidman, J., Khouri, H., Craven, B., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Submitted (01-MAR-2000) The Institute for Genomic Research, 971:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="peptide ABC transporter, periplasmic peptide-binding protein, putative" /protein_id="AAF38391.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydophila pneumoniae AR39.
Chlamydophila pneumoniae AR39
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 11764)
                                                                                   2453 TCTACAAACATAGAACAAGAAGAACATCACCAAAAACGCTCGGAATTAG 2502
                                                                                                                                                                                                                                                                                              2403 CCATCAGGAGTTCCTCCTTATGCAATCAACCATAAGGACTTCCTAGAAAT 2452
                                                                                                                                                                                          2503 TGTCGCAAGCTTCTCTTTACCTAGAGACCTTTCATATTATGAGCCGATC 2552
                                                    467 eLeuGlnAsnIleGluGlnGluGlnAspHisGlnLysArgSerGluLeuV 484
                                                                                                                                                              484 alSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIleGluProlle 500
                                                                                                                                                                                                                                                                     501 TyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAsnLeuGl 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="synonym: Chlamydia pneumoniae AR39"
complement(109. .1707)
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                                                                                                                                                                                                                                                                                                                                                                                                        2603 AGTCTCACCAACAGGAGTTGTGGACTTCCGTTATGCTAAGGAAAAT 2648
                                                                                                                                                                                                                                                                                                                                                                            517 yValSerProThrGlyValValAspPheArgTyrAlaLysGluAsn 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="AR39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE002216 AE002161
AE002216.2 GI:8163460
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SOURCE

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LSKNPHYYNQSQVETKTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQ
                                      SKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHL
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LASRAHLHIFPQYINKALQQANLLIEDMDLIAVTQTPGLIGSLSVGVHFGKGIAIGAK
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INBYFRSAIQTACNLPVYFPPAKLCSDNAAMIAGLGGENFOKNSSIPEIRICARYQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:M17532 SP:P15282 GB:X13968 PID:145356 PID:443307; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="G1:7189486"
//teaslation="MKKYYIDBALKEILRLEGAATQEELCAKLLAQGFATTQSSVSR
WLRKIQAYKYAGRESTEKTTEHLVLSIHHNASLIVTTVPGSASWIAAL
LDGGLKDEILGTLAGDDTIFVTPIDEGREPLLAVSTANLLQYFLD"
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AENINGGINSLSIGQWESAMYLGYKYQIFVYIIYPQVFKNILPSLTNEFVSLIKESS
ILMVVGVPELTKVTKDIVSRELNPMEMYLICAGLYFLMTTSFSCISRLSEKRRSYDN"
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LRALAGLVQPTQCDIWIEGEAPALVFQQPELFSHWTVLGNCTHPQIHIKGRSFEERRE
KAFELLHLLDIEEVAKNYPDQLSGGQKQRVAIVRSLCMDKHTLLFDEPTSALDPFATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="amino acid ABC transporter, ATP-binding protein" /protein_id="AAF38394.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFRHLLETLRDQELTVGLTTHDMQFVHSCLDRIYLIDQGTVAGVYDKRDGELDSGHPL
                                                                                                                                                                                                                                                                                                                                          endopeptidase; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="amino acid ABC transporter, permease protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CP0575"
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similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                          match to PFAM protein family HMM PF00814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="arginine repressor"
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                                                                                                                                                                                                                                                                                                                                   /note="0-sialoglycoprotein
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                                                                                                                                                                                                                                                             complement(1653, .2687)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:7189488
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3263. ,3916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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3906. AFR
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2771. .3214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start≈
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34

gene

CDS

to: 11764

from: 1

Percent Identity: 100.000

Length: Gaps: 20

29

84

us-09-824-567-2.rge

CDS

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1707 ATGCGCAAGATATCAGTGGGAATCTGTATCACCATTCTCCTTAGCCTCTC 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAACTCGCTATTAATATAAGAGATGAACCCCGTTCTTTAGATCCAAGA 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1507 ATTAGTTCAAGAAAATAATCTTTCAGGAAATATAGAGCCTGCTCTTGCAG 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1157 TITICCCGTTCATAAATCTCAAAGAACCTGCAATCCAAATCTCTACCT 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 SerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPhelleGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 uSerTrpLysGlnValAlaThrGlnGluValSerGlylleTyrAlaPheA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 IleAspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 ysThrIleThrIleHisPheIleProAspAlaAsnThrAlaAlaLysLeu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetArgLysIleSerValGlyIleCysIleThrIleLeuLeuSerLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 IlealaSerGlyalaPheTyrProLysAsnIleLysGlnLysGlnTrpIl
                Glimmer2; putative"
                                                                                                                                                                                                                                                                                                               to reverse of: AE002216
                                            /codon_start=1
                                                                                                                                                                                                                                                          US-09-824-567-2 x AE002216/rev
                                                                                                                                                   Ratio: 5.148
Percent Similarity: 100.000
                                                                                                                       Quality: 2739.00
                                                                                              alignment_scores
                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                               Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1057
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                                                                                                                                                                                                                                                                                                                                           YRVIGLGEPKNGEDAVSKDYLERYVSSQLTIDKVEDKPITKPNKGKLLYSQGTSPKLE
GPLPLGLLTSGISGFTWKSASKSNDGSPPFSALRHKETESDTDCROITSTLLSGNQAG
TYTWSLSLKVLVPSIRQIEKPEVQLSLVYSYEDWLPIDNIFNWSQPRIIPLALLGQTM
LAGGKYDILBLAAHQINQTLMISPNCSRFSLQLKQTNQFENSPVDFYIVHAAHSCHWS
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KESGLSCSAEELKISWFGRQTARKIKLTGEAKDEVFSAERFELDGSLLRLLIYKKPKG
ITLSGWSLKINEPASIDHPSVSHLDPGSLLTYLNDCKIISFHGFITMKTVSGSSLSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFYLEKSSERFWIKCVVSEDQOSGNIFIESVLSPDVSISAOFSSVPVAFFRIFIASPFWDLLLSYEDIINLSAEATHTNDGKISMTASGBGNQYQMKLQGHIHKSTFYIVEGSSSFIELKPELASALCNQIIPLSTPITSKQIHATVSYAKIPLDITWKHIEITSQAQLPEVAIHPKDPNIALQLRDTKLGIKKTEKFSDIRYSSSTVLGGASPSHLNGLISIDNKKHIJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FREQOAQLPHTYLRAIPPOPPTINVPEDVAYYSLNIBGTYKNAHLEADAILDNPILKE
SCSWSGAMKNFLFKGQGTYHFNKKWQEILSPHFSYABARFSGKAQTTDTNLFPKFSG
KITARENBELLIHAKFGSPNEPIKPETTSILIHGQFCSLPESLVSNHLAPPHLKKLFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHTDGGKFVTKGNIQALIENPDYPDLANTRILIPDILLSLDESSTSPSSKDLKTGGSG
EIFSLPLDSITKTYGKQVRLSPYFGSSGDLAPVVNYNPKDONKLTLLSNFKSEALLGE
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PEETKGLSCLTLLAAGGLEGSLEATFLIFYDNVSKETFIINDFKGSLRANNLDAKIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLKGSCLAPRQDSKTLAEFSLEGQVDHLFSPESREFKQTANWIHIPSSFIAGIIPMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLKAQISSLAĞPRINVSIKNAFREGEGPVDIMVDSENLQAQIPLILNEKSILLRENLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHLSINEDVNKAFLQEFNPLLAGGAYSQYPYTLEIDKQNFYLPIRPYSFEEFRIOSAT
LDMGKISLANTGTMYALFQFLDITDQKQFVESWFTPIFFSVQKGSIICKRXDALIDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRLALMGKTDIAHDRLFWTLGIDPEVIKKYFHNTSIKTKNFFLIKIRGSISSPEVDWS
SAYARIALLKSYSLGNPFSSLADKLFSSLGDSTPPPTVHPFPWEKSNFDSIENK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVLSYIGLLICVPILVFFLRLSQHLFTNLNWKEMLIIKFPDYKRPIVATVEAAYHATE
SNIGLVLVGSFFVFCWAGILMLLSLEDGLNKIFRTSWTFISLKRLVSYFVITLVSPMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MFRKLFPFSKKKTGQKQRLRNNGLLQAIIQSIKVLLHNEAXKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIIVCGSWITITQIMPIQYAKLFSLSHSMTALYFISRFVPYLLIYLALFCCYAFLPRY
AIQKTSALISTLIIGSVWIVFQKAFFSLQVSIFNYSFIYGALVALPSFLLLLYIYMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLFGGALTFIIQNRGCTFIFLGDKILPSCYLQLITSTYILALTTROFNEGLSPLPAOF
IARQSKVPIGEVSQCLDVLEKEGFLFPYNNGYQPVFNFSELTIKDIADKLLHREIFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="conserved hypothetical protein; identified by Glimmer2; putative"
                                                  /note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="conserved hypothetical protein; identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="conserved hypothetical protein; identified by
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.5978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(9494. .10786)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(6069. .9497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6069. .9497)
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/transl_table=11
                                                                                                                                        /transl_table=11
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/transl_table=11
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                              CP0577
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gene

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section 1/4.
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808
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                                                                                                                                                                                                                                                                                                      AlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGl 367
                                                                                                                                                                                                                                                                                                                       uLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProV 384
                                                                                                                                                                                                                                                                                                                                                                     alSerSerSerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrp 400
                                                                                                                                                                                                                                                                                                                                                                                                                       LysGluSerLeuGlyPheAlaIleProIleValGlyLysGluPheAlaLe 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 uLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 TCTCCAAGCAGCACTATCTTCAGGGAACTTCTCTTTTAGCTACAGGAGGAT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 ProSerGlyValProProTyrAlaIleAsnHisLysAspPheLeuGlu11 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCAGGAGTTCCTCCTTATGCAATCAACCATAAGGACTTCCTAGAAAT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eLeuGlnAsnIleGluGlnGlnGpAspHisGlnLysArgSerGluLeuV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIleGluProIle 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTACAAAACATAGAACAAGAGCAAGATCACCAAAAACGCTCGGAATTAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisL
                                                  eProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerP
                                                                                                  heAspValAlaGlyThrSerTrpLeuThrPheAsnIleAsnLysPhePro
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                                                                                                                                                                   euLeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAsnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 yValSerProThrGlyValValAspPheArgTyrAlaLysGluAsn 532
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AL Submitted (04-UUL-2000) Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1 Minamikoquahi, Ube, Yamaguchi 755-8505, Japan (E-mail:mahiraigeo.cc.yamaguchi-u.ac.jp, Tel:81-836-22-227, Fax:81-836-22-2415) On Aug 31, 2000 this sequence version replaced gi:6172286 gi:6172328 gi:6172312 gi:6172314 gi:6172314 gi:6172316 gi:635165 gi:655164 gi:655164 gi:655165 gi:655165 gi:655165 gi:655165 gi:655167 gi:655167 gi:655167 gi:8547422 Ab033780-Ab033781, Ab033792-Ab033792-Submitted (14-Feb-2000) Ab03845-Ab038847: Submitted (18-Dec-2000).

COMMENT

Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K., Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T. Comparison of whole genome sequences of Chlamydia pneumoniae J138

Nucleic Acids Res. 28 (12), 2311-2314 (2000)

(bases 1 to 299650)

Direct Submission

AUTHORS TITLE JOURNAL

MEDLINE

JOURNAL REFERENCE

TITLE

Shirai,M. 20330349

from Japan and CWL029 from USA

Chlamydophila pneumoniae J138 (strain:J138) DNA. Chlamydophila pneumoniae J138 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.

(sites)

REFERENCE AUTHORS

ORGANISM

KEYWORDS

SOURCE

/ERSION

GI:9956082

AB038347 BA0000008

ACCESSION

AP002545.2

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seq_name: gb_ba:AP002545
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BCT 08-DEC-2000

LOCOS AP002545 299650 bp DNA linear BCT 08-DBI DEFINITION Chlamydophila pneumoniae J138 genomic DNA, complete sequence,

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CDS

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CDS

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Location/Qualifiers

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source

FEATURES

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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCTGLPGSLPVLNOSAVEKAVLFGCAVEGEISLLSRFDRKSYFYPDSPRNFQITQFEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYKYFPEPLLPTLOLTESYIERIRKTLPELPYDKYHRYIQEYGLSEDIASILISDKNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLSAEKGTTIFGGRETSLPFLNGTHLLONARFLKLOARNGYSIEFYDPTTSEDGGSTU
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KHQIRVVRSSLKAMVPEFLDIRRIFEEEFFFLSARKRLIDLATTLVERKILTEDLER
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                                                                                                                                                                                                                                                       KVLESDLEGILAQTESAESLLTQEELPILATRGALEKAVFKGSLCCALASKAKPYFEE
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                                                                                                              NAVLLEKVIYRSLQKSYRDIGMSSAKMKILHGNPFFSLEDNKKTIMKEHAEMLESLSS
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DFRMALEAMOFNEEALLOEELSIQAPSE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIEMTLRWYELPLLFMKNTFERASLOYNSCKEMLAKVEPQCKESPTYRSSOERLERLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKRSVKEVMDRFMRVTWKSWEASVMLDHSYGVARELFKKAVGVLEESVYKILFKSYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEKERSNENQRKVKDVEKWLSKGLAEFRNQESRRARERLRELQTLYPEVSVEERVLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLEDCLETWSKKLTKAEESVFEMKFDATEKLGNKVLSDVTNRLEILCEDAEEMIFRIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 rValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 532
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Ratio: 5.148
Percent Similarity: 100.000
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| 233954 | 67 234004 | 84 234054 | 100 234104 | 117 234154 | 134 234204 | 150 234254 | 167 234304 | 184 234354 | 200 234404 | 217 | 234504 | 250 | 267 234604 | 284 | 3470 | 317 234754 | 334 | 350 234854 |
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| 5 GAGAACTCGCTATTAATATAAGAGATGAACCCCGTTCTTTAGATCCAAGA | 1 GlnvalargLeuLeuSerGlulleSerLeuVallysHislleTyrGluGl | 7 yLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaG | 4 luaspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLys | 1 SerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGl | 7 uSerTrpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheA | 4 laLeuAsnProlleLysAsnValArgLysTleGlnGluGlyHisLeuSer | 1 IleaspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh | 7 rLeugluSerProThrSerHisPheLeuLySLeuLeuAlaLeuProValp | hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro | . ilealaSerGlyAlaPheTyrProLysAsnileLysGlnLysGlnTrpil | etysLeuSerlysAsnProHisTyrTyrAsnGlnSerGlnValGluThrt | ysThrIleThrIleHisPheileProAspalaAsnThrAlaAlaLysLeu | PheAsnGlnGlyLysLeuAsnTrpGlnGlyProProTrpGlyGluArgll | eProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerP | heaspvalaiaglythrSerTrpLeuthrPheasnIleasnLysPhep | LeuasnasnmetiysLeuargglualaLeualaSeralaLeuaspiysGl | ualaLeuValSerThrIlePheLeuGjyargalaIysThralaaspHisL | euLeuProThrAsn11eHisSerTyrProGluHisGlnLysGlnGluMet |
| 23390 | 233955 | 23400 | 234055 | 101 | 117 234155 | 134 | 151 234255 | 167 234305 | 184 234355 | 201 | 217 | 234505 | 251 234555 | 267 234605 | 284 234655 | 301 23 4 705 | 317 234755 | 334 |

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BCT 30-0CT-2000
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Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Glimwood,J., Davis,R.W. and Stephens,R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis science 282 (5389), 754-759 (1998) 99000809 9784136
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AE001293.1 GI:3328597
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Stephens.R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R.,
Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q.,
Koonin,E.V. and Davis,R.W.
235105 GGTTCGCAGACTTTGCTGATCCTATGGCATTTCTAACGATCTTTGCTTAT 235154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235305 TACCACGACTITCAATTIGCTAIGGATAAAAACTITCTAATCTAGG 235354
                                                                                                                                                                                                                                                                                                                                                                                                                          434 rpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr 450
                                                                                                                                                                                                                                                                                        434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 alSerGinAlaSerLeuTyrLeuGluThrPheHisIleIleGluProlle 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 TyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAsnLeuGl 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235355 AGTCTCACCAACAGAGTTGTGGACTTCCGTTATGCTAAGGAAAAT 235400
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Chlamydia trachomatis
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                        uLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProV
                                                                                                                                                                                                                                                                                417 uLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 yvalSerProThrGlyValValAspPheArgTyrAlaLysGluAsn 532
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10192388
3 (bases 1 to 11944)
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IAPVYTYPPMDARTVICVVTSILLPIFSIVRMLYNIFRFFIVPFYILFOMVRONYOTD
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NNDVIRSKGWOFFFEERNYMFEGGGFRSGLGONAWYLLGCFOPVQLFLLKDGVIISGA
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WSNGDLITAHDFVRSWNDVLQNRVASIYSFAFLPIDVNKDSGFFAKDDHTLVINLLTP
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SGTSWLTFNTAKKPFSHSKLRQALSLVLNKEALASLAFVKPAKHLLPAHLHTYPEQPS
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Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R., Aravind, L., Mitchell, W.P., Olinger, L., Tatusov, R.L., Zhao, Q., Roonin, E.V. and Davis, R.W. Direct Submission Submission Submission of Calman in Infectious Diseases, University of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
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complement(105. .878)
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6780 CICCAGCIACTCACACACATIGCIGIAAGCGIAAAAGATGATCCTCGCACA 6829
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Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T.,
Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,
Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE002315 12173 bp DNA linear BCT 26-MC Chlamydia muridarum, section 46 of 85 of the complete genome.
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On Jun 1, 2000 this sequence version replaced gi:7190506.
Location/Qualifiers
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7988 TCCATTTTCTCC...TCGAAAGGAGTCAAACCTTATGCTTTACAAGATCC 8034
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                                                                                                                                                                                                                                                                                                                                                                            479 ysArgSerGluLeuValSerGlnAlaSerLeuTyrLeuGluThrPheHis 495
                                                                                                                                                                                                                                                                                                                                          496 IleIleGluProlleTyrHisAspAlaPheGlnPheAlaMetAsnLysLy 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:83560"
/note="synonym: Chlamydia trachomatis MoPn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia muridarum
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 12173)
                                              446 ThrilePheAlaTyrProSerGlyValProProTyrAlaIleAsnHisLy
                                                                                                                                                 462 sAspPheLeuGluIleLeuGlnAsnIleGluGlnGluGlnAspHisGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                           512 sLeuSerAsnLeuGlyValSerProThrGlyValValAspPheArgTyrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae AR39
Nucleic Acids Res. 28 (6), 1397-1406 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Chlamydia muridarum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="TC0464"
complem=
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/gene="TC0464"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE002315 AE002160
AE002315.2 GI:8163226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .12173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8235 CTAAAAACTCT 8245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_ba:AE002315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 laLysGluAsn 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIDHSNIPLMFCNITHLINHPGARAVAMGGLAGFIGRNAPTITDSGGGGJFSLAYGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGEHSQDLTSIVSAYNPIDLAYRVSCLPSDSRSILYKSLDSIASKIAFIINTDSASRW
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NTAGRLMTNEFFAFLMETTVKEVATCIRNNPGVDLTRLVFVLDFKGELQGFVTDRSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IASPEMPLKQIMRPVEHKVLADTTREEVVDLVERYKVAVLPVVDEENFLIGAITYEDY
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4208. .4366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:7190509"
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/gene="TCO466"
/note="magnesium transporter; identified by match to TIGR
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                                                                                                                                                                                                                                                                                  /note="similar to GB:AL009126; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4208. .4366
/gene="TCO467"
/note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="conserved hypothetical protein; identified by
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/transl_table=11
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/protein_id="AAF39316.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein family HMM TIGR00400"
/codon_start=1
                                                                                                                                                      complement(1227. .2345)
/gene="TC0465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAF39317.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4328. .5410)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                               VSKTSADRASSED"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TC0468"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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CDS

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/note = similar to GB:M57689 SP:P24139 GB:X56347 PID:143606
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/protein_id="AAP39321.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7133 ACGITIGACCCICGAGAGGITAGGCITCITICGGATATIAATITGATICA 7182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7183 CCAICTTATGAGGGACTGGTTCAAGAGACTCCT...TCCGGAGGGTTT 7229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7230 TCCCTGCATTAGCAGAAGTTTCTTCCTATCTGAAGATAAGAAAACCTAC 7279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7330 TCATGATTTTGTACGTTCTTGGAACGATGTTTTGCAAAATCGCATTGCAA 7379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7409 .....GATTTAAGTAAAGAT...TGTGGATTCTTCGCTAAGGACAATCA 7449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 aGluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValSerG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 lylleTyrAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGln 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetArgLys1leSerValGlyIleCys1leThr1leLeuLeuSerLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 rValValLeuGlnGlyCysLysGluSerSer......HisS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 GluGlyHisLeuSerIleAspHisPheGlyValHisSerProAsnGluSe 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 rThrLeuValValThrLeuGluSerProThrSerHisPheLeuLySLeuL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 sHisIleTyrGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 euAlaLeuProValPhePheProValHis...LysSerGlnArgThrLeu 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 erSerThrSerArgGlyGluLeuAlaIleAsnIleArgAspGluProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 luProAlaLeuAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrPheLysLeuLysSerAlaPheTrpSerAsnGlyAspProLeuThrAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 49.442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1 to: 12173
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9618. .10481
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                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1345.00
Ratio: 3.135
ilarity: 79.740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AE002315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-824-567-2 x AE002315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                           gene
                                                                                                 CDS
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VIRSRGIWGIFCEKNCLLEGGGTRSGLGQHAWYLLGCFQPFRLFLLKDGEIVSGARPS
IQAFPENNEYLTSYLYGAALGRLTSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TETRIES ALLON "MRKVGVGICLLIALATAITGGSKSSSNKSNHSSSNGSVGVSNKD
DPRTPEPREVELLSDINLIHHLYEGLVQETPSGEVFPALAESFELSEDKKTYTFHLKK
ALMSNGDLITAHDEVPSKNWYLODNIALSIYSFELPIDLSSCOGFFARDNITHIUNINH
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STFSYIKILIPELAGSICLLIGALILAGTITTVPAIAASYFLSIGVTLVVAGIGLCSV
FRPHLFSINQSQDLHIIYY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MLTLGLESSCDETSCALVENGKILANRIASQDIHAAYGGVIPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLESLCLALRGGTTLGTLAAFYKRGGGRTTFFSSTIQISVPAFVIGAFLQYIFAIKYS
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LIKHVLPVALFPVISYSAFLITTLATGTFSIENLFCIPGLGKWFICSIKQRDYPMTLG
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                                                                                                                                                                                                                      /note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="peptide ABC transporter, periplasmic peptide-binding protein, putative" //protein_id="AAR39319.1" //db_xref="G1:7199512".
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/gene="TC0469"
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8668, 9612
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gene

CDS

us-09-824-567-2.rge

| 211 eLysC 7600 AAAAC | ebysGlnLysGlnTrplleLysLeuSerLysAsnProHisTyrTyrAsnG ::::::: | 228 7649 |
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| 245 AsnT] :::1 7700 CAGA(| ASTTATALAALALYSLEUPHCASNGINGIYLYSLEUASNTTFGINGIYPT ::: :: | 261 7749 |
| 261 oPro 111 7750 ICCE | OPTOTINGLYGLUARGILEPTOGLINGLUThTLEUSERASNLEUGLINSETL | 278 |
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PAT 06-FEB-2002
                                                                                                                                                                                                                                           chlamydophila pneumoniae.
Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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122 ATCCTGGAAAACTCGTCTCATTGCAGACCAAACTCTAATGCGTCATCTA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 ysLeuLysSerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAsp 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 PhelleGluSerTrpLysGlnValAlaThrGlnGluValSerGlylleTy 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 rAlaPheAlaLeuAsnProlleLySAsnValArgLySIleGlnGluGlyH 148
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Ratil, G. and Grandi, G.
Ratil, G. and Grandi, G.
Immunisation against Chiamydia pneumoniae
Patent: WO 0202606-A 128 10-JAN-2002;
Chiron S.p.A. (IT)
Location/Qualifiers
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DEFINITION Sequence 128 from Patent W00202606.
VERSION AX349605.1 GI:18615409
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ORGANISM
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ORIGIN
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TITLE
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us-09-824-567-2.rge

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AE002215 12980 bp DNA linear BCT 30-MAY-2000 Chlamydophila pneumoniae AR39, section 43 of 94 of the complete
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Bubmitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA

Do Jun 1, 2000 this sequence version replaced gi:7189472.

Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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/protein_id="AAF73687.1"
/db_xref="G1:8163459"
Chlamydophila pneumoniae AR39
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                         461 HisLysAspPheLeuGluIleLeuGlnAsnIleGluGlnGluGlnAspHi 477
                                                                                                                                                                                                                                                                                                                                                                        511 LysLysLeuSerAsnLeuGlyValSerProThrGlyValValAspPheAr 527
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complement(197. .1609)
/gene="CP0560"
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/organism="Chlamydophila pneumoniae AR39"
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                                                                                                                                                                         477 sGlnLysArgSerGluLeuValSerGlnAlaSerLeuTyrLeuGluThrP
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AE002215.2 GI:8163458
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PUBMED
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JOURNAL
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VESCHTLACSSTELINDYLEEMEKWLEDFPIEP"
COMPLEMENT(2487. .2684)
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ALLGSRPQAVEKAVREISPAFFSIPKKYQLIRIDTPKDDAPSILFPIGIEIILKDLCI
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                                                                                                                                                                                                                                                                                                                                                                                  Glimmer2; putative<sup>r</sup>
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complement(5946. .6800)
/gene="CP0567"
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11663 GTAGGCCAAGAGTITTTCACAATACAAAAACTICCTAGAGGGGAACTA 11614
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11313 TTTTAFAGAAAA 11301

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179
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Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                                                                                                                                                                    | 1 (sites) | Ratti.G. and Grandi.G. | Immunisation against Chlamydia pneumoniae | Immunisation against Chlamydia pneumoniae | Patent: WO 0202606-A 28 10-JAN-2002; Chiron S.p.A. (IT) | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | /organism="Chlamydophila pneumoniae" | /db_xref="taxon:83558" | /db_xref="taxon:8358" | /db_xref="taxon:83
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A249505
DEFINITION Sequence 28 fr
ACCESSION AX349505
VERSTON AX349505
KEYWORDS
SOURCE Chlamydophila
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ORIGIN
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Murdin,A.D., Oomen,R.P., Wang,J. and Dunn,P.
Chlamydia antigens and corresponding dna fragments and uses thereof
Patent: WO 0185972-A 1 15-NOV-2001,
Aventis Pasteur Limited (CA)
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                                                                                                                                                                    1501 ATTACGCTATACATCCTAAAATCCAGAATACATTGGGATCTCTTCTAGG 1550
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Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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2.116
68.391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-824-567-2 x AX300389
                                                                                                                                                                                                                                                                                                                   seq_name: gb_pat:AX300389
                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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FEATURES

TITLE

SOURCE

CDS

ORIGIN

sednence

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YHRKDLSHRYIYDYDHGKINKTPRKIQCSSNHHSLATSKTSCSSRKILRARRTGSSYR
RPIAQQELITFISAQQKTNSNPLKSICKFIDRTHQNLHIQVFCFNHPTIIQHLVKAAA
REVRVSVQYRDGTELEBACKDSTICLQKQSGRSLFHKKSNVGDSQRVLASSGNFTPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEQDINLSLLINDSELARHIETNOFVTROIGNOFLYYPPIFRRNDSCAFFANTIKKUI
AQAKKTIVVVYILTHPVILKSLQAAARGVKVEVAVDTRESEOTORTLERLOLSLPL
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WQSYBEKTERLIAGASLKRPREEEDDPGGGTSSGISSAGASAKRAKTQ*
complement(1661. 3049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /traislation="mydrkfefilogislltselsddfpctrglpkadihyhld
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QQNIRIAYVIYPSEKPLEARLKLYDLFSRASQLFLSQGITLRFLNGFNKTGSSNLQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MCSPCPRHLFPIVTDCPTCSTPPLRKRPLSSTTAAAVVVTQLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQQREERAAWLDERASFPULEVGLQSAGAESCPEAAPTKLTSGYHHAYENGFGCEA
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FSADEDSHLTHYTSSPLTFKEIIQLNVEAIVSSFVDVDTKIMLLNSIHEYLSTYLKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="rc0442"
/note="similar to GB:M10101 SP:P04079 PID:146276 GB:U00096
PID:1788854; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVLLGLSGGVDSSVLAVLLHNALGDRLSCVFVDTGLLRKNEVEEVKOOFSSLGLEILV
VDASEKFEHLLSG1EDPEQKRKVIGAAFIEVFDEASKNLDVQWLAQGTIYSDVIESAK
SCDATOVIKSHHNVGGLPEKALNKLLEPLRFLFNEDVARLGKVLGLFVVLISRHEFPG
PGLGFRVLGEVREEVELYKNADSIFIEELKKANLYHKVSQAFAFLPCKSVRYKGDC
RHYGYTIALRAVESTDFWTACWPSLSREFLNRCSSRIINEIPEVCRVVYDISDKPPRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSGLIFSGGPHSVYQNNSPEVDKEIYNSNIPILGVCYGMQLIARDFGSEVQGGKSEFG
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KKLFGLQFHPEVSDSQDIGDKILSNFVKHICQTSETWKIETIEKQLIQGIREKVGETE
                       Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Direct Submission

Submitted (01-WaR-2000) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TCC11""/potherical protein; identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                   similarity; putative" (codo_start=1)
                                                                                                                                                                                                                                                                                                               /note="synonym: Chlamydia trachomatis MoPn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="phospholipase D family protein"
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/db_xref="G1:7190485"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="GMP synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1661. .3049)
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complement(3064..4602)
                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                    /gene="TC0440"
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Chlamydia muridarum, section 44 of 85 of the complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 11402)
Read,T.D., Brunham,R., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
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Read,T.D., Brunham,R., Shen,C., Gill,S.R., Heidelberg,J.F.,
                                                       1131 TCAATCTTCAAAAGAGATCTCAACAGAAGAAGGACAAAAGAAAAGCCAGA 1180
                                                                                                                                                                                                                                                                        1225 CGCAGAACTCAGCATCCTCTATAGATTCCTCGAATTCCTCCATCA 1274
                                                                                                                                                              1181 GCATATTTTCAAGAAGCTAAAGAAACACTT.....TCTGAAAAGAACT 1224
                                                                                                                                                                                                                                                                                                                                                                            1325 AAAATCCAAGGCATGGAGTACCACTGCTTTTTAAAGAAACGTCGTCAAGG 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1425 TAGCCTTCCTATCTATTCTAGGCAACCCCAGAGACCTCACAATGG... 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1472 ...AGAAACAGTGATTACGAAAAGACTTTAGAGAAACTCTATCTCCCTCA 1518
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342 yrProGluHisGlnLysGlnGluMetAlaGlnArgGlnAlaTyrAlaLys 358
                                                                                                                                                                                                                                                                                                                                      392 euValGlnLeulleArgGluGlnTrpLysGluSerLeuGlyPheAlalle 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 ProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSerGl 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425 yAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaAspProM 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 etAlaPheLeuThrIlePheAlaTyrProSerGlyValProProTyrAla 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 uGlnGluGlnAspHisGlnLysArgSerGluLeuValSerGlnAlaSerL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 euTyrLeuGluThrPheHisIleIleGluProIleTyrHisAspAlaPhe 505
                                                                                                            359 LysLeuPheLysGluAlaLeuGluGluLeuGlnIleThrAlaLysAspLe
                                                                                                                                                                                                                         375 uGluHisLeuAsnLeuIlePheProValSerSerAlaSerSerLeuL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1556 ....ATAGAAGAAGAAACCCCGATTATCCCCCTGTATCACGGCAAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1601 ATTTACGCTATACATCCTAAAATCCAGAATACATTCGGATCTCTTCTAGG
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AE002313.1 GI:7190484
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CGUREQIVAINNATSSIOIGMCILTHRGILQALNBAATQRSVLVTIIIDSLESQOTI
DILKALGSKLRYKYGTGDRIHCKACILDHNTAIIGSANWAASGLKANKEDIIIVNPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="conserved hypothetical protein; identified by Glimmer2; putative" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7390 ....CTAAGAAATATTTTGCGTGTTGCCTATTTGCCACGATGCAATGTCTT 7435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1436 TAGATCCTCGCCAAGTTTTTTTGATTAAAGATGTTTGTATAGCAAAAGCA 7485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7630 GATTITGAAGAGTCTATAAAGCAATTTTATCTCCATGAGGTTGATAATGT 7679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 heLysLeuLysSerAlaPheTrpSerAsnGlyAspProLeuThrAlaGlu 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LeuSerLeuSerValValLeuGlnGlyCysLysGluSerSerHisSerSe 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 oAlaLeuAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrP
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Gaps: 12
Percent Identity: 35,305
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                                                                                                                                                                                                                                                                                                complement(10175. .10582)
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                                                                                                                                                                                                                                                                                                                                             complement(10175. .10582)
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                                                                                                                                                                                                                                                                    MDSVTELSNATAMSVAGGLGTVHKNMDVNAQVATVKQIKSQSTSSVIGGAVGIGQQGL
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SQDFLYDYPVLNCTVLFCNVNHKPLDNPSLRAALSLAIDRETLLKLAGKGSIATSFVH
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QOLEDVLGFKISTLGLEYHSFLDKRSKGEFSLSTGNWVADYQOAKAFLSILGNOTKY
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                                                                        GB:U00096; identified by sequence similarity; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identified by sequence similarity; putative"
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Chlamydia trachomatis section 18 of 87 of the complete genome.
AE001291.1 GI:3328573
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Nonin, E.V. and Davis, R.W.

Direct Submission
Submitted (20-MAY-1998) Program in Infectious Diseases, University of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
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Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 1082).
Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R., Aravind, L., Mitchell, W.P., Olinger, L., Tatusov, R.L., Zhao, Q., Koonin, E.V. and Davis, R.W.
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                                                                                                                                                                                                                                                                    487 laSerLeuTyrLeuGluThrPheHisIlelleGluProlleTyrHisAsp 503
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Science 282 (5389), 754-759 (1998)
99000809
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LOCUS AE001291
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PUBMED
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|------------------------|---|--|---|--|
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| alignment Percent | <pre>int_scores: Quality: Ratio: it Similarity:</pre> | 685.50 2.071 62.928 Percent | Length: 526 Gaps: 10 | |
| alignment US-09-824 | _block: -567-2 x | AE001291 | | |
| Align | seg 1/1 to: A | AE001291 from: 1 | to: 10827 | |
| 1 419 | 4 0 | <pre>'ValValLeuGlnGlyC ::: 'TTTGGGCTAACATCTT</pre> | LeuSerLeuSerValValLeuGlnGlyGysLysGluSerSerHisSerSe::: | e 30 . 4237 |
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| 47 | | lnValArgLeuLeuSe AGGTTTTTTAAGCAA | euAspProArgGlnValArgLeuLeuSerGluIleSerLeuValLysHis | 63 4333 |
| 64 4334 | | LeuValGlnGluAsnA: ::: :::: TTAGTCCGGGAAAAGG | IleTyrGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluPr | 80 |
| 8(437E | 0 oAlaLeuAlaGlu | uAspTyrSerLeuSer! AAGATATCATCAATCT | OAlaLeuAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrP | 97 4427 |
| 4428 | 7 heLysLeuLysSe : 8 TTTTCTAAAAA | eralaPheTrpSeras; ::::: | helysleulysseralaphetrpserasnglyaspproleuthralaglu | 113 4477 |
| 114 | A - 0 | SerTrpLysGlnValA] :: CTATTAACAAATTT | AspPhelleGluSerTrpLysGlnValAlaThrGlnGluValSerGlyll | 130 4527 |
| 130 4528 | | aLeuAsnProlleLys# : CTTGCATTAATTAAAA | eTyrAlaPheAlaLeuAsnProIleLySASnValArgLysIleClnGluG | 4 10 |
| 147 | | .eAspHisPheGlyVal :::: !TGAAGATTTAGGTGTT | 1yHisLeuSerIleaspHisPheGlyValHisSerProAsnGluSerThr | 163 4627 |
| 164 | | JeuGluSerProThrSe ::: TAGAAAACCCGTTTCC | LeuValValThrLeuGluSerProThrSerHisPheLeuLySLeuLeuAl | 180 4677 |
| 180 | | PheProValHisLyss:::!!!!!!! | aLeuProvalPhePheProvalHisLysSerGlnargThrLeu | 194 4727 |
| 195 | | rLysSerLeuProlle :::: ACGCGTTTTCCCGATA | GlnSerLysSerLeuProlleAlaSerGlyAlaPheTyr :::::::: | 207 4777 |
| 208 | | ysGlnLysGlnTrpIl. :::::::::: AGCCGCAAAGATATTT | ProLysasnileLysGlnLysGlnTrpIleLysLeuSerLysAsnProHi:::::::::::::::::::::::::::::::::::: | 224 4827 |
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                                                                                                                                                                                                                                                                                                                            ||||
| 5025 TITIATTCTGTAACATTCAACAACACCTTTAAATAATCCCCCGGGGAG 5074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5460 CTAGTGCTTTCCTGTCCTAGGT.....AAT 5488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 pLeuGluHisLeuAsnLeullePheProValSerSerSerAlaSerSerL 391
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5589 TTATGGCAGAGCAGTTGTTGCTTAAAGAAAGTCCTCTTATTCCTCTATAC 5638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 IleProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSe 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 rGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaAspP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 roMetAlaPheLeuThrIlePheAlaTyrProSerGlyValProProTyr 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 AlaIleAsnHisLysAspPheLeuGluIle.....re 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 uGlnAsnIleGluGlnGluGlnBspHisGlnLysArgSerGluLeuValS 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 erGlnAlaSerLeuTyrLeuGluThrPheHisIleIleGluProlleTyr 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502 HisaspalaPheGlnPheAlaMetasnLysLysLeuSerAsnLeuGlyVa 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518 lSerProThrGlyValValAspPheArg 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
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5689 CTCTTCTCGTGGAGAAATTGATTAAAA 5716

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4083. 515
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3161. .4078
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                                                                                                                BCT 06-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mkkrwsivtlmilfptlvlsacgfggggsngbgkdskgkttlni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVKAVNDKTLKVELNNPTPYFTELTAFYTYMPINKKIAEKNKKWNTNAGDDYVSNGPF
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CGTPFETHFCRLLHILGPWAAQVLTGSFIIETIFGIPGIGAHFVNSITNRDYTVIMGV
TVFFSVILLLCVLIVDVLYGIIDPRIKLSKAKKGA"
                                                                                                                                                                                                 SpoOK operon; oligopeptide permease; sporulation protein.
B.subtilis (strain JH642) DNA, clones pDR20/21, pJL2/3 and pJL7.
Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                              Rudner, D. 2., LeDeaux, J. R., Ireton, K. and Grossman, A. D. The spook locus of Bacillus subtilis is homologous to the oligopeptide permease locus and is required for sporulation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="alternative translation start"
                                                                                                                                                                                                                                                                                               Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 173 (4), 1388-1398 (1991)
                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="sporulation protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sub_strain="JH642"
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2222. ,315
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                                                                         seq_documentation_block:
                            seq_name: gb_ba:BACSPOOK
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91139580
                                                                                                     BACSPOOK
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TITLE
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                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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| | | | 26 | 35 | 20 0 | 68 697 | 85 | 101 | 117 | ന്ത് | 150 | 167 | യ്റ് | 200 | KO 5t | 227 | 243 | 9 |
|---|-------------------|-----------|--|----------------------------------|--|--|---|--|---|--|--|---|--|--|--|--------------------------------|--|-----------|
| Length: 540 Gaps: 13 entity: 29.444 | | 300 | leThrIleLeuLeuSerLeuSerValValLeuGlnGlyCysLysGluSe :: ::::: :::::: ::::: TCACGTTGATGCTCACTCTCGTGCTGAGCGCGTGCGGCTTTGG | SerHisserserThrSerargGlyGlu | LeualaileasniieargaspGluproargSerLeuaspProArgGln | Valargleuleusergluileserleuvallyshisiletyrgluglyle | alGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluA ::::: ::: ::: CACGTATCAATGCAGATGGTGAGCTGAAGAAGGCATGGCTTCTA | SPTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSer | AlapheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGl ::: GGTGTGAAAIGGTCTAATGGAGACCCTGTAACTGCACAAGATTTGAATA | uSerTrpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheA ::: TGCTTGGAAATGGGGGGTTGACCTAATAATGAATCACAATACGCTTACC | laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer | IleaspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh ::: :: :: | rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP ::::: | rGlnArgThrLeuGlnSerLysSerLeuPro | SerGlyalaPheTyrProLysasnIleLysGlnLysGl | nTrp | snGlnSerGlnValGluThrLysThrIleThrIleHisPheIleProAsp::::::::::: ::: ::: ::: | nG1 |
| Len G nt Ident | | 1 to:6 | 7alLeuGl :: FTGCTGAG | AAAGGACA | oArgSer | alLyshi: :::::: TCCGTCA(| IlegluPı CCTGAAG | rTyrThrE ATATACAT | euThrAla :: FAACTGCA | ValSerGl ::::: AATGAATC | slleglng ::: GCGAATA | anGluSer ::::: \TGACAAA | ysteute ::// :aattaac | LeuGlns. :::: .GAGAAA | nn | erLysAsı :: AAAAAA | ThrileHi ::: GATATGG1 | nGlyLysI |
| Percer | : | from: 1 | uServalv ::::::! cacrcrcc | rgGlyGlu :: :: | AspGluPr ACTGAGCC | SerLeuv :::::: | erGlyasn :: ::: \TGGTGAG | lyteuth GAAAGAC | AspProLe | rGlnGlu' ::: CCCTAATA | alArgLys :::: CTGAAGCC | SerProAs ::: GCTGTGAA | SPheLeuI : :TTCACTG | lnArgThr :: AAATTGCA | ProLysas ::: STATCAAA | eLysteus : ACTCTCG | SThrile GAAAATC | heAsnGlı |
| 617.50 1.735 65.926 | ACSPOOK | BACSPOOK | SeuSerLe | rThrSera :::::: AAACGGTG | snileArg, ::: \TATTAAA | erGluile ::: TATCAGG | Asnteuse ATGCAG | rSeraspG ::: CAAGGACG | erAsnGly | ValAlaTh ::: GCGCTTGA | eLysAsnV :::: AAAAGGTG | lyvalhis :: CAGTAAAA | PhrserHi :: ACTCCATA | LysSerG | aPheTyr] \TGATTAT | Ile | GluThrLy ::: AAACTGAA | aLysLeuF |
| <pre>Scores: Quality: Ratio: Imilarity:</pre> | ock: 67-2 x BA | /1 to: B, | ThrileLeu ::::: ACGTTGATG | rHisSerSer ::: CAGCGGATC | eualailea TAACATIA | rrgLeuLeuf :: ATGATTCAG | GlnGluAsr ::: .CGTATC | rSerLeuse ::: TGAAACGAG | heTrpS TGAAATGGT | TrpLysGln TGGAAATGG | uAsnProIl CTACTACAT | spHisPheG | 3luSerPro :::::: AATAACCGG | hePheProValHisLysSerGlnArg' ::::: :::: aTATGCCGATCAATAAGAAAATT | aSerGlyAl::: | NACACAGGG | SerGlnVal | nThrAlaAl |
| ાં જે ાં | ent_blo -824-5 | seg 1, | 0 B | 7 N | ω œ | _ | | 5 spry 5 aaar | | | | _ | | hePhe | IleAla | nTrp. ATGGA | snGln ::::: ATAAA | AlaAs |
| 11gnmen Percent | lignme US-09- | Align | 1 49 | 54 | 3 293 | 52 | 69 698 | 745 | 102 795 | 117 | 134 | 151 | 167 995 | 184 | 201 | 215 | 227 | 244 |

1292 TATGCCGCTCGGACAG...CTTCCGACAGAATCCCTGCCGACCCTGAAAA 1338 ||||||| | 1389 TTCAACACTGAAGCTAAAGCCATTAGACAACGTCAATATCCGTAAAGCTTT 1438 1539 GATAACAAGGATACTTCAAAGACAATGATGTCAAAACAGCAAAAGA 1588 260 yProProTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuGlnS 277 277 erLysGlyHisLeuHisSerPheAspValAlaGlyThrSerTrpLeuThr 293 294 PheasnileasniysPheProLeuAsnasnMetLysLeuArgGluAlale 310 1589 ATACCTIGAAAAAGGCCTAAAAGAATGGGCTTAAGCAAGGCATCTGATT 1638 310 uAlaSerAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyA 327 327 rgAlaLysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyrPro 343 344 GluHisGlnLysGlnGluMetAlaGlnArgGlnAla...TyrAlaLysLy 359 1686 ATCGCTCAAGCAGTACAAGAAATGTGGAAGAAAAATTTAGGCGTTGATGT 1735 1786 AAGATFATCAAATCGGCCGTATGGGCTGGCTCGGCGACTTCAATGATCCT 1835 359 sLeuPheLysGluAlaLeuGluGluLeuGlnIleThr...AlaLysAspL 375 375 euGluHisLeuAsnLeuIlePheProValSerSerSerAlaSerSerLeu 391 392 LeuValGlnLeulleArgGluGlnTrpLysGluSerLeuGlyPheAlaIl 408 408 eProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSerG 425 425 lyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaAspPro 441 1033 TIGGGTACAGGATGAAAACCTAAAAGGTGTTATCATGCCAGGTACTGGTG 2082 442 MetalaPheLeuThrIlePheAlaTyrProSer...GlyValProProTy 457 457 ralalleAsnHisLysAspPheLeuGlulleLeuGlnAsnIleGluGlnG 474 474 luglnAspHisGlnLysArgSerGluLeuValSerGlnAla...SerLeu 489 490 TyrLeuGluThrPheHisIleIleGluProIleTyrHisAspAlaPheGl 506 506 nPheAlaMetAsnLysLysLeuSerAsnLeuGlyValSerProThrGlyV 523 2083 AGGITTATITCAGAAACGCA 2102 523 alValAspPheArgTyrAla 529

seq_name: gb_pat:AX027646

Fri Jul 26 08:37:38 2002

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|--|--|---|---------------------------------------|---|---|---------------------------------|----|---|--|------|--|--|
| seg_documentation_block: LOCUS AX027646 DEFINITION Sequence 1 ACCESSION AX027646 VERSION AX027646.1 GI.10188535 KEYNORDS SOURCE Hacillus subtified | NISM Bacillus Subtliss Bacteria: Firmicutes; Bacillus/Clost Bactlus/Staphylococcus group; Bacillus/Caphylococcus group; Bacillus/Caphylococcus group; Bacillus/Staphylococcus group; Bacillus/Staphylococcus group; Bacillus ORS Diaz-Torres,M. and Ferrari,E. Froduction of proteins in gram-posit No 0039333-A 1 06-JUL-22000; DIAZ TORRES MARIA (US); FERRARI EUG Location/Qualifiers Jurce Location/Qualifiers Location/Qualifiers | Adams Subliss Sublist | alignment_scores: Quality: 617.50 | Align seg 1/1 to: AX027646 from: 1 to: 6300 | 10 lleThrileLeuLeuSerLeuSerValValLeuGlnGlyGysLysGluse 26 ::: ::::: ::::: ::::: | 26 rSerHisSerSerThrSerArgGlyGlu | 51 | 52 ValArgLeuLeuSerGlulleSerLeuValLysHisIleTyrGluGlyLe 68 :::::::::::::::::::::::::::::::::::: | 85 SPTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSer 101 745 AAATTGAAAGGAGGAGGAAGGAAGACATATACCATTCGTGAT 794 | | 134 laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer 150 | |

1045 ATATGCCGATCAATAAG...AAAATTGCAGAGAAAAATAAAAGTGGAAT 1091 1092 ACAAATGCCGGAGATGATTATGTATCAAAGGGGCCGTTCAAAATGACGGC 1141 184 hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro 200 1142 ATGGAAACAGCGGCTCTATTACTCTCGAAAAAATGACCAGTATTGGG 1191 201 IleAlaSerGlyAlaPheTyrProLysAsn.....IleLysGlnLysGl 215 167 rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP 184 244 AlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGlnGl 260 260 yProProTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuGlnS 277 277 erLysGlyHisLeuHisSerPheAspValAlaGlyThrSerTrpLeuThr 293 294 PheasnIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLe 310 1539 GATAACAAAGGAGGATACTTCAAAGACAATGATGTGAAAAGAAGAAAAGA 1588 310 uAlaSerAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyA 327 327 rgAlaLysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyrPro 343 344 GluHisGlnLysGlnGluMetAlaGlnArgGlnAla...TyrAlaLysLy 359 359 sLeuPheLysGluAlaLeuGluGluLeuGlnIleThr...AlaLysAspL 375 1736 GAGCTIGATAACTCAGAGIGGAATGICLATATTGATAAGCTCCACAGCC 1785 ::: ||||||| :::|||| 1836 ATCAACTTCCTTGAATTGTTCCGGACAAAAGGGAGAAATAACGATAC 1885 392 LeuValGlnLeuIleArgGluGlnTrpLysGluSerLeuGlyPheAlaIl 408 375 euGluHisLeuAsnLeuIlePheProValSerSerSerAlaSerSerLeu 391 408 eProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSerG 425 425 lyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaAspPro 441 442 MetalaPheLeuThrIlePheAlaTyrProSer...GlyValProProTy 457 457 ralalleasnHisLysAspPheLeuGluIleLeuGlnAsnIleGluGlnG 474 215 nTrp.....lleLysLeuSerLysAsnProHisTyrTyrA 227 snGlnSerGlnValGLuThrLysThrIleThrIleHisPheIleProAsp

- 1886 AGGCTGGGAAAATCCAGAATTCAAAAAGCTTCTGAATCAGTCACAAACTG 1935
 - 523 alvalAspPheArgTyrAla 529 ||| |||||| ||| 2083 AGGTTTATTTCAGAAACGCA 2102

OM of: US-09-824-567-2 to: N_Geneseq_032802:*

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Ratio: 5.148
Percent Similarity: 100.000
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US-09-824-567-2 x AAD20238
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2.8e-30
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| SIDS5/grgdata/geneseq/geneseqn-embl/NA1999.DAT.BAX91990 + 2726.00 4779.32 |
| SIDS5/grgdata/geneseq/geneseqn-embl/NA1999.DAT.BAS1875 + 755.50 1323.26 |
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                                                                                                                             About: Results were produced by the GenCore
Copyright (c) 1993-2000 Compugen Ltd.
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Database: N.Geneseq_032802;*
Database sequences: 1736436
Database length: 85845721
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/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX20051 + 321.50 550.92 2.4e-22 /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT.AAX20050 + 321.50 550.91 2.4e-22 /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAX20050 + 321.50 500.71 2.4e-22 /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:ABA03041 + 321.50 500.77 1.5e-19 /SIDS5/gcgdata/geneseq-geneseqn-embl/NA2002.DAT.ABA03041 + 309.00 438.27 4.6e-16 /SIDS5/gcgdata/geneseqn-embl/NA2001A.DAT:ABA03041 + 309.00 438.27 4.6e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding cassette; antibiotic; vaccine; infection; therapy; poxvirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for preventing or treating Chlamydia infection e.g. infection caused by C. trachomatis, C. psittaci, C. pneumoniae or C. pecorum in mammals, such as humans. The nucleic acid molecules are useful for producing ArP-binding cassettes, in the construction of vaccine vectors such as poxylruses, which are further useful for preventing and/or treating chlamydia infection and in the construction of attenuated Chlamydia strains that can over-express the nucleic acid molecules or express than nucleic acid molecules or express chlamydia pneumoniae ATP-binding cassette.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cassette protein and its corresponding gene. Sequences of the invention are useful for detecting Chlamydia infection by assaying a body fluid of a mammal with the components. They are also used as vaccines. ATP binding cassette antibodies and vaccines of the invention are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Chlamydia ATP-binding cassette and corresponding DNA molecule f
preventing, diagnosing and treating Chlamydia infections in mammals,
                                                                                                                                                                                                                                              seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD20238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "ATP-binding cassette protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1799 BP; 560 A; 439 C; 294 G; 506 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae ATP-binding cassette gene.
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101.,1699
/*tag= a
                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAD20238 standard; DNA; 1799 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2001; 2001WO-CA00455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2002 (first entry)
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Percent Identity: 100.000

to: 1799 from: 1 to: AAD20238 Align seg 1/1

- 1 MetArgLysIleSerValGlyIleCysIleThrIleLeuLeuSerLeuSe 17
- 34 17 rValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgG
 - 50 34 lyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArg
- 201 51
- 29 GlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGl
 - 84 yLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaG 67 301
- - 117 SerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGl 101
- 450
 - 134 uSerTrpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheA 117
- 134 laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer 150 167 151 IleAspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh CCTTGAATCCAATTAAAAATGTACGAAAGATCCAAGAGGGACACCTCTCC 501
 - 900 551 167
- 601
 - hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro 200 651 184

yValSerProThrGlyValValAspPheArgTyrAlaLysGluAsn 532

517

501 TyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAsnLeuGl

- IleAlaSerGlyAlaPheTyrProLysAsn1leLysGlnLysGlnTrp11 201
- eLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrL 217
- ysThrIleThrIleHisPheIleProAspAlaAsnThrAlaAlaLysLeu 234 801
- 251 PheasnGlnGlyLysLeuasnTrpGlnGlyProProTrpGlyGluargIl 267
- eProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerP 284 267 901
- heAspvalAlaGlyThrSerTrpLeuThrPheAsnIleAsnLySPhePro 300 284

951 ITGATGTCGCAGGAACCTCATGGCTCACCTTCAATATCAATAAATTCCCC 1000 .051 AGCICITGICICAACIATATICITAGGCCGIGCAAAACIGCCGAICAIC 1100 1300 317 uAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisL 334 367 uLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProV 384 384 alSerSerAlaSerSerLeuLeuValGlnLeulleArgGluGlnTrp 400 417 rpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr 450 434 484 alSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIleGluProlle 500 LeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGl AlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGl LysGluSerLeuGlyPheAlaIleProIleValGlyLysGluPheAlaLe 417 uLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyT 301 351 401 434

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss. Nucleotide sequence of the complete genome of Chlamydia pneumoniae. seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX91990 ВР seq_documentation_block: ID AAX91990 standard; DNA; 1230025 13-SEP-1999 (first entry) AAX91990;

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(GEST) GENSET

Griffais R;

WO9927105-A2

20-NOV-1998; 04-NOV-1998; 21-NOV-1997;

03-JUN-1999.

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245380 CTCAACAATAIGAAGCITAGAGAAGCCITAGCAICAGCCITAGATAAGGA 245429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245530 GCACAACGCCAAGCTTACGCTAAAAACTCTTTAAAGAAGCTTTAGAAGA 245579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245580 ACTCCAAATCACGCTAAAGATCTCGAACATCTTAATCTTATCTTTCCG 245629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245680 AAAGAAAGTTTAGGGTTCGCTATCCCTATTGTCGGAAAGGAATTTGCTCT 245729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 uLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProV 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 euLeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMet 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 uLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyT 434
                uSerTrpLysGlnValAlaThrGlnGluValSerGly1leTyrAlaPheA
                                                 244830 ATCTTGGAAACAAGTAGCTACTCCAAGAAGTCTCAGGAATCTATGCTTTTG
                                                                                                                         244880 CCTTGAATCCAATTAAAATGTACGAAGATCCAAGAGGGACACCTCTCC
                                                                                                                                                                       134 laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 eLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ysThrIleThrIleHisPheIleProAspAlaAsnThrAlaAlaLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 PheAsnGlnGlyLysLeuAsnTrpGlnGlyProProTrpGlyGluArgIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 AlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGl
                117
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                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY3584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244480 ATGCGCAAGATATCAGTGGGAATCTGTATCACCATTCTCCTTAGCCTCTC 244529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 yLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetArgLysIleSerValGlyIleCysIleThrIleLeuLeuSerLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 1
Percent Identity: 99.812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 1230025
                                                                                                                                                                                                                                                                                                                                      Genome, sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 291-611; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                          98US-0107078.
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Ratio: 5.124
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Chlamydia pneumoniae.
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alignment_scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
245980 TACCACGACGCATTTCAATTTGCTATGAATAAAAAACTTTCATAATCTAG 246029
                                                                                                                                                                                                                                                                 seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NN1999.DAT:AA201425
                                                                                                                                                      ProSerGlyValProProTyrAlaIleAsnHisLysAspPheLeuGluIl 467
                                                                                                                                                                                                                                                                                                                          484 alSerGlnalaSerLeuTyrLeuGluThrPheHisIleIleGluProlle 500
                                                                                                                                                                                                                                                                                                                                                                                                            501 TyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSer.AsnLeuG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246030 GAGTCTCACCAACAGAGTTGTGGACTTCCGTTATGCTAAGGAAAT 246076
                                                                  rpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 lyValSerProThrGlyValValAspPheArgTyrAlaLysGluAsn 532
                                                                                                                                                                                                                                        eLeuGlnAsnIleGluGlnGluGlnAspHisGlnLysArgSerGluLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence of Chlamydia trachomatis.
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97FR-0015041.
97FR-0016034.
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17-DEC-1997;
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epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in
                                                                                                       Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       252009 CICCAGCIACICACACAGIIGCIGIAAAGGIAAAAGAIGAICCICGCACA 251960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251642 TCTTGTTATCAATCTCCTCACTCCAACTCCACATTTTCTAAAGCTGCTTA 251593
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                                                                                                                                                                                                                                                                                                                                                                                          1 MetArgLysIleSerValGlyIleCysIleThrIleLeuLeuSerLeuSe 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 rValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 sileTyrGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 leTyrAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 rLeuValValThrLeuGluSerProThrSerHisPheLeuLysLeuLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 roAlaLeuAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 PheLysLeuLysSerAlaPheTrpSerAsnGlyAspProLeuThrAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 uAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValSerGlyI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyHisLeuSerIleAspHisPheGlyValHisSerProAsnGluSerTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251592 CCCTCCCCGTATTTTATCCTGTGCAT...TCGCAGCATCAGATATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 GlnSerLysSerLeuProlleAlaSerGlyAlaPheTyrProLysAsnIl
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Gaps: 10
Percent Identity: 50.278
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                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AAZ01425
                                                                                                                                                                                                                                                                                                   US-09-824-567-2 x AAZ01425/rev
                                                                  treating these diseases.
                                                                                                                                                                                                                            3.146
79.963
                                                                                                                                                                                                  Quality: 1356.00
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251145 GCAAAA......CATCTCCTTCTTCTTCTTTTCACACCTACCCAGA 251105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251054 TAGAAGATCTCTGACTGACTTAACATGACTATTAAGGATCTAGAGAAA 251005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250904 GCGGGAAAGATATGCTTTGTTGCAAACGATCTAATAGGCAATACTTTC 250855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250757 ATCCTCAATTTGATCAACTGATTCTCTCTATAGAACGGAAAAAACCCT 250708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250707 CAAAAACGCTCAGCTTTAATTTCCGAAGCTTCTCTATACATAGAAAGACA 250658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250657 AAACGICATAGAACCCCTCIATCACGACGTGIICCATTATACAACAATA 250608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 oProTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuGlnSerL 278
228 InSerGlnValGluThrLysThrIleThrIleHisPheIleProAspAla 244
                                                                                                                                                                                                                                                                                            278 ysGlyHisLeuHisSerPheAspValAlaGlyThrSerTrpLeuThrPhe 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 aSerAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyArg. 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 uHisGlnLysGlnGluMetAlaGlnArgGlnAlaTyrAlaLysLysLeuP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 heLysGluAlaLeuGluGluLeuGlnIleThrAlaLysAspLeuGluH1s 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nLeulleArgGluGlnTrpLysGluSerLeuGlyPheAlalleProlleV 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 alGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSerGlyAsnPhe 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 eLeuThrIlePheAlaTyrProSerGlyValProProTyrAlaIleAsnH 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 isLysAspPheLeuGluIleLeuGlnAsnIleGluGlnGluGlnAspHis 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 GlnLysArgSerGluLeuValSerGlnAlaSerLeuTyrLeuGluThrPh 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 eHisIleIleGluProIleTyrHisAspAlaPheGlnPheAlaMetAsnL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 ysLysLeuSerAsnLeuGlyValSerProThrGlyValValAspPheArg 527
                                                                                                                                                                                                                                                                                                                                                                                          295 AsnileAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAl
                                                                                              245 AsnThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 AlaLysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyrProGl
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The present invention relates to the isolation of Chlamydophila pneumoniae strain CWL029 genes and their encoded proteins. The genes of the invention encode an ATP binding cassette gene, a secretary locus open reading frame (ORF), an endopeptidase, a protease, a protease, a protease, a cup protease ATPase, a CLP protease Submit, a transglycolase/transpeptidase, a CLP protease, or thioredoxin. The genes of the invention can be used in a vector as a vaccine for the prevention and treatment of Chlamydia infections. Also described are B- and T-cell epitopes from the proteins of the invention which can be used as Chlamydia antigens. AAS18750-AAS18759 represent the C. pneumoniae
                                                                                                                                                                                                                                     ATP binding cassette; secretary locus open reading frame; endopeptidase; secretary locus ORF; protease; metalloprotease; CLP protease ATPase; CLP protease subunit; transglycolase/transpeptidase; CLPc protease; thioredoxin; Chlamydia infection; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine useful for immunising mammals against chlamydia infections, comprises vectors having sequences of ATP binding cassette gene, secretary locus open reading frame gene of chlamydia
                                                                                                                                                                                                     Chlamydophila pneumoniae gene encoding an ATP-binding cassette.
                                                          seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:AAS18750
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                                                                                                                BP
                                                                                                                                                                                                                                                                                                                    Chlamydophila pneumoniae CWL029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 355pp; English.
                                                                                                           AAS18750 standard; DNA; 1787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-207852P.
2000US-211796P.
2000US-211797P.
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2000US-211801P.
2000US-212044P.
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2000US-235361P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AVET ) AVENTIS PASTEUR LID
                            250557 TATGCTAAAACTCT 250543
                                                                                                                                                                      26-MAR-2002 (first entry)
528 TyralaLysGluAsn 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oomen RP,
                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-049447/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU09430.
                                                                                                                                                                                                                                                                                                                                                    WO200185972-A2.
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16-JUN-2000;
16-JUN-2000;
16-JUN-2000;
26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000;
16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2000;
26-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murdin AD,
                                                                                                                                          AAS18750;
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Length: 522 Gaps: 9 Percent Identity: 33.908

755.50 2.116 68.391

Percent Similarity:

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Quality:

alignment_scores:

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292 euThrPheAsnIleAsnLysPheProLeuAsnAsnMetLysLeuArgGlu 308

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Opp operon; SpoOK; oligopeptide permease; sporulation; ABC transporter; ATP-binding cassette transporter; mutation; protein production; oppA; oppD; oppF; ds.
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1181 GCATATTTTCAAGAAGCTAAAGAAACACTT....TCTGAAAAAGAACT 1224
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                                                                                                                                                                                                                                                                                                                                                                                        1275 TAGCTCAAGAATCCAAAGACAACTTAAAGATACCTTAGGATTGAAATC 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1325 AAAATCCAAGGCAIGGAGTACCACTGCITITIAAAGAAACGTCGTCAAGG 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1472 ...AGAAACAGTGATTACGAAAAGACTTTAGAGAAAACTCTCCCTCA 1518
                                                                                                                                                                                                         342 yrProGluHisGlnLysGlnGluMetalaGlnArgGlnAlaTyrAlaLys 358
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                                                                                                                                                                                                                                                                                   359 LysLeuPheLysGluAlaLeuGluGluLeuGlnIleThrAlaLysAsple 375
                                                                                                                                                                                                                                                                                                                                                            375 uGluHisLeuAsnLeuIlePheProValSerSerAlaSerSerLeuL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                        392 euValGlnLeuIleArgGluGlnTrpLysGluSerLeuGlyPheAlaile 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 ProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSerGl 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 IleasnHisLysAspPheLeuGluIleLeuGlnASnIle.......Gl 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 yAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaAspProM 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 etalaPheLeuThrIlePheAlaTyrProSerGlyValProProTyrAla 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 uGlnGluGlnAspHisGlnLysArgSerGluLeuValSerGlnAlaSerL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 euTyrLeuGluThrPheHisIleIleGluProlleTyrHisAspAlaPhe 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  506 GlnPheAlaMetAsnLysLysLeuSerAsnLeuGlyValSerProThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAA51864 standard; DNA; 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 yValValAspPheArg 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. subtilis opp operon.
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to: AAA51864 from: 1 to: 6300

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The opp operon of Bacillus (also known as spook operon) encodes an oligopeptide permease that is required for the initiation of sporulation and the development of genetic competence. The opp operon is a member of import or export of oligopeptides from 3-5 amino acids. Bacillus strains containing a mutation in the opp operon produce more recombinant protein than the wild-type strain. Therefore, gram-positive microorganians, genes of the opp operon can be used for heterologous protein production, genes of the opp operon can be used for heterologous protein production, growth factors or cytokines.
                                                                               /product= ligand-binding_protein
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/note= "this codon contains an apparent 1 base deletion
which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of proteins, such as hormones, enzymes, growth factors or cytokines, in gram-positive microorganisms containing a mutation in at least one of the genes of the opp operon gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY97040, AAY97041, AAY97042, AAY97043, AAY97044.
                                                                                                                                                                   membrane_protein
                                                                                                                                                                                                                  membrane_protein
                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1A-M; 32pp; English.
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                                                                                                                                                                                                   /label= oppc
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/label= oppF
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4083.,5159
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                                                                                                                                                                             161..4078
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5152..6078
                                                                                                                                                                   product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrari E;
                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMV ) GENENCOR INT INC
                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                       DIAZ-TORRES M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-452412/39
           Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                FERR/) FERRARI E.
                                                                                                                                                                                                                                                                                                                             WO200039323-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diaz-Torres M,
                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                     36-JUL-2000
                                  Key
                                                                                                                              CDS
                                                                                                                                                                           CDS
                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                       CDS
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Sequence 6300 BP; 1919 A; 1222 C; 1462 G; 1697 T; 0 other;

Gaps: 13
Percent Identity: 29.444

1.735 65.926

Percent Similarity:

US-09-824-567-2 x AAA51864

alignment_block:

617.50

Quality:

alignment_scores:

Ratio:

Length:

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10 IleThrIleLeuLeuSerLeuSerValValLeuGlnGlyCysLysGluSe 26
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                                                                                                                                                                                                                                                                                                                                                                           85 spTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSer 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 AlaPhe...TrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 laLeuAsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSer 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1092 ACAAATGCCGGAGATGATTATGTATCAAACGGGCCGTTCAAAATGACGGC 1141
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195 GGTGTGAAATGGTCTAATGGAGACCCTGTAACTGCACAGATTTTGAATA 844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            845 IGCTIGGAAATGGGCGCTTGACCCTAATAATGAATCACAATACGCTTACC 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 AACAATACGGAACTAAAAATTCCAAGCTGGCGAACTTGATTGGGCCGG 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 ..LeualalleAsnIleArgAspGluProArgSerLeuAspProArgGln 51
                                                                                                                                                                                                                                                          52 ValArgLeuLeuSerGlulleSerLeuValLysHisIleTyrGluGlyLe 68
                                                                                                                                                                                                                                                                                                                                              68 uValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 IleAspHiSPheGlyValHisSerProAsnGluSerThrLeuValValTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      945 CTAGACGATGTGGCAGTAAAAGCTGTGAATGACAAAACGCTGAAGGTTGA 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 hePheProValHisLysSerGlnArgThrLeuGlnSerLysSerLeuPro 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 nTrp.....IleLysLeuSerLysAsnProHisTyrTyrA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 yProProTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuGlnS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 erLysGlyHisLeuHisSerPheAspValAlaGlyThrSerTrpLeuThr 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  895 AGCICTACTACATAAAAGGIGCIGAAGGGGGAATACCGGAAAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 snGlnSerGlnValGluThrLysThrIleThrIleHisPheIleProAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 ilealaSerGlyAlaPheTyrProLysAsn.....IleLysGlnLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 AlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGlnGl
                                                                                     rSerHisSerSerThrSerArgGlyGlu............
                                                                                     26
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Antigenic protein; vaccine; Lyme disease; infection; detection; ss.

Borrelia burgdorferi.

WO9859071-A1

Lathigra R;

Hanson MS,

97US-0050359. 97US-0053344. 97US-0053377.

98WO-US12718. 97US-0057483

18-JUN-1998; 30-DEC-1998

03-SEP-1997 20-JUN-1997; 22-JUL-1997; (HUMA-) HUMAN GENOME SCI INC

(MEDI-) MEDIMMUNE INC Erwin AL,

Choi GH,

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1339 AAGACGGTTCTTTACATGTTGAGCCGATTGCAGGAGTGTATTGGTACAAA 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX61764
                                                                                          1389 TICAACACTGAAGCTAAGCCATTAGACAACGTCAATATCCGTAAAGCTTT 1438
                                                                                                                                                                         1489 AGCAAATCCCGGCAATGGCTGCAGCCCTACAATGAAGGGATTTGAG 1538
                                                                                                                                                                                                                                                                                                                                                                        1539 GATAACAAAGAAGGATACTTCAAAGACAATGATGTCAAAACAGCAAAAGA 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 PheAsnIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLe 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1639 TGCCAAAAATCAAATTGTCTTACAAC...ACTGATGACGCACACGCGAAA 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1686 ATCGCTCAAGCAGTACAAGAAATGTGGAAGAAAATTTAGGCGTTGATGT 1735
                                                                                                                                         310 uAlaSerAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyA 327
                                                                                                                                                                                                                                   rgAlaLysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyrPro 343
                                                                                                                                                                                                                                                                                                                            GluHisGlnLysGlnGluMetAlaGlnArgGlnAla...TyrAlaLysLy 359
                                                                                                                                                                                                                                                                                                                                                                                                                      359 sLeuPheLysGluAlaLeuGluGluLeuGlnIleThr...AlaLysAspL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1836 ATCAACTICCIIGAAIIGIICCGCGACAAAAACGGAGAAAIAACGAIAC 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 euGluHisLeuAsnLeuIlePheProValSerSerAlaSerSerLeu 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1886 AGGCIGGGAAAAICCAGAAIICAAAAAGCIICIGAAICAGICACAAACIG 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eProlleValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSerSerG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 lyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaAspPro 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1986 TICATIGAAAAIGCCG...GTIGCCCCAAICIATITCIAIACIGAIAC 2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2033 TIGGGTACAGGATGAAAACCTAAAAGGTGTTATCATGCCAGGTACTGGTG 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 MetalaPheLeuThrIlePheAlaTyrProSer...GlyValProProTy 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 ralalleasnHisLysAspPheLeuGlulleLeuGlnAsnlleGluGlnG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 luGlnAspHisGlnLysArgSerGluLeuValSerGlnAla...SerLeu 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuValGlnLeuIleArgGluGlnTrpLysGluSerLeuGlyPheAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506 nPhealaMetasnLysLysLeuSerAsnLeuGlyValSerProThrGlyV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 TyrLeuGluThrPheHisIleIleGluProIleTyrHisAspAlaPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAX61764 standard; DNA; 1536 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 alValAspPheArgTyrAla 529
                                                                                                                                                                                                                                   327
                                                                                                                                                                                                                                                                                                                              344
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This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                          to develop
                                                                                                                                                                                                                                                                                                                                                                                             New isolated Borrelia burgdorferi nucleic acids - used to develc
products for the diagnosis, prevention and treatment of diseases
caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 TAAIGTCGCATCAAAAATGATTGACACAATGTTTAGAGGGATTGTTACAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 GAGATCCTAATACAGGGGGAAATAAACCGGGACTTGCAAAAGGGTGGGAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 LeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSerAlaPhe.. 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 .TrpSerAsnGlyAspProLeuThrAlaGluAspPhelleGluSerTrpL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 TTGGAGTGACGGAGTTGCAATCACTGCAGAAGGAATTAGAAAATCTTATC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ysGlnValAlaThrGlnGluValSerGlyIleTyrAla...PheAlaLeu 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 TTAGAATTTTAAATAAAGAAACTGGCTCAAAGTACGTTGAAATGGTTAAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 IleAsnIleArgAspGluProArgSerLeuAspProArgGlnValArgLe 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 ATAAGCTIGGGAGCAGAGCAAGCAGTCTTGACCTCAATTAGCAGAGGA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 uLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeuValGlnG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1536 BP; 631 A; 246 C; 256 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 luAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAspTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 485
Gaps: 15
Percent Identity: 28.041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: AAX61764 from: 1 to: 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 182-183; 275pp; English.
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64.330
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US-09-824-567-2 x AAX61764
                                                                                                                                                                                                                                                                                                                                            WPI; 1999-189980/16.
                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY20067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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B. burgdorferi antigenic protein coding sequence, t606.nt.

19-JUL-1999 (first entry)

AAX61764;

A S X E X E X

| 36 AsnProlleLysAsnValArgLysI ::: 43 TCGGTAATTAAAAATGGTCAAAAAT | ### SECTION OF THE PROPERTY SECTION SE |
|---|--|
| 152 pHisPheGlyValHisSerProAsnGluSerThrLe:::::::: :::: | GluSerThrLeuValValThrLeuG 169 ::: GAAAAACATTAGAAATAACACTGG 442 |
| 169 luserprothrserHispheLeulysLeuLeuala | <pre>Leu 181 ::Tradracaccaarcarratr 492</pre> |
| 182 ProvalPhePheProValHisLysSerGlnArgThrLeuGlnSerLysS | Lysse 19 :: TGGAC 53 |
| 198 rLeudrolleAlaSerGlyAlaPheTyrProLysAsnIl:: | YAlaPheTyrProLysAsnileL 212 |
| 212 ysGlnLysGlnTrpIJ6LysLeuSerLysAsnProHis ::::: | lin 2: |
| 229 SerGinvalGluThrLysThrIleThrIleHisPheIleProAsp :::::: :: :::: 637 AATGAAGTAGAAGAGATTACATTTTACACAACAATGAC | IleHisPheIleProAspalaas 245 ::::: :::: TTTACACAACAAATGACAGCIC 686 |
| 245 nThralaalaLysLeuPheAsnGlnGlyLysLeuAsnT: | YLysLeuAsnTrpGlnGlyProP 262 ::: ::: AGAGCTAGATGCAA 727 |
| 262 roTrpGlyGluArgIleProGlnGluThrLeuSerAsnLe 1:: :: 728 TTTTGGTTCCATACCCCCAGATCTAATCAAAATCT | uGlnSe ::: AAAAT |
| 279 GlyHisLeuHisSerPheAspValAlaGlyThrSerT ::: ::: 775 AGGACTATTACTCATCAGCTGTTAATGCCATATACT | AlaGlyThrSerTrpLeuThrpheAs 295 ::: ::: ::: ANGCCATATACGTTCAA 824 |
| 295 nileAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLee :::: | LysLeuArgGluAlaLeuAlas 312 ::: ::: AAAATAGAAAGCCTTAACTC 874 |
| 312 erAlaLeuAspLysGluAlaLeuValSerThrIleph | <pre>srThrilePheLeuGlyArgAla 328 ::: ::::: vTAAAAGTTCTTCACAACGG 921</pre> |
| 329 LysThralaAspHisLeuLeuProThrasnIleHisS | SerTyrProGluHi 34. |
| 345 sGlnLysGlnGluMetAlaGlnArgGlnAlaTyrAla ::: 964TCTTATGCA | LysL 3. ::: TTAGAAT 9 |
| AlaLeuGluGluLeu ::: SAAATTGCAAAAACC | ThrAlaLysAspLeuGlu 37 ::: GCTGAAGCTGGATATCTT 10 |
| 377 HisLeuAsnLeullePheProVal | AAAATACAATACAAAGGA 108 |
| 387 rAlaSerSerLeuLeuValGlnLeulleArgGluGln? | IleargGluGlnTrpLysGluSert 404 |
| 404 euGlyPheAlaIleProlleValGlyLySGluPheAlaLeuLeuGlnAla ::::: ::: :::::::::::::::::::::::::: | SGluPheAlaLeuLeuGlnAla 420 :::::: AGAATGGACAAACATACTTANAAC 1103 |

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This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic protein; vaccine; Lyme disease; infection; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS5/gcgdata/geneseq/geneseqn·embl/NA1999.DAT:AAX61763
                          1233 TTATGCTGATCCTTTGACATTTTTAAGCATATTCACA......CAAGGAT 1276
                                                                                                                                                       1277 ACACACAATTCTCATCATAATTACTCAAACCCAGAATACAACGAACTT 1326
                                                                                                                                                                                                                1327 ATAAAGAAATCCGACCTTGAGCTTGATCCAATAAAAAGACAAGACATTT 1376
                                                                                                                                                                                                                                                                        421 AspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAs 437
                                                                                                                         454 alProProTyrAla.....IleAsnHisLysAspPheLeuGlulle 467
                                                                                                                                                                                      468 LeuGlnAsnIleGluGlnGluGlnAspHisGlnLysArgSerGluLeuVa 484
                                                                                                                                                                                                                                                   484 lSerGlnAla...SerLeuTyrLeuGluThrPheHisIleIleGluProI 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. burgdorferi antigenic protein coding sequence, f606.nt.
                                                              PPheAlaAspProMetAlaPheLeuThrIlePheAlaTyrProSerGlyV
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                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID AAX61763 standard; DNA; 1587 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970S-0050359.
970S-0053344.
970S-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                     1427 TATAC 1431
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22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09859071-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX61763;
                                                              437
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Sequence 1587 BP; 648 A; 251 C; 259 G; 429 T; 0 other;

|||::::::
94 ATAACTTGGGAGCAGAGCAGTCTTGACCCTCAATTAGCAGAGGA 143 194 GAGATCCTAATACAGGGGAAATAAACCGGGACTTGCAAAAGGGTGGGAT 243 LeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSerAlaPhe.. 103 104 .TrpSerAsnGlyAspProLeuThrAlaGluAspPhelleGluSerTrpL 120 ||||||:::||| 294 TIGGAGIGACGGAGITGCAAICACIGCAGAAGAAAITAGAAAAICITAIC 343 ysGlnValAlaThrGlnGluValSerGlyIleTyrAla...PheAlaLeu 135 54 uLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeuValGlnG 71 71 luAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAspTyrSer 87 344 TTAGAATTTTAAATAAAGAAACTGGCTCAAAGTACGTTAGAATGGTTAAA 393 136 AsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSerIleAs 152 PHisPheGlyValHisSerProAsnGluSerThrLeuValValThrLeuG 169 ||||||||| 494 AATCACCAAAACCTTATTTTATTGATATGTTAGTACACCAATCATTTATT 543 169 luserProThrserHisPheLeuLysLeuLeuAla......Leu 181 182 ProvalPhePheProvalHisLysSerGlnArgThrLeuGlnSerLysSe 198 198 rLeupro.....IleAlaSerGlyAlaPheTyrProLysAsnIleL 212 212 ysGlnLysGlnTrplleLysLeuSerLysAsnProHisTyrTyrAsnGln 228 229 SerGlnValGluThrLysThrIleThrIleHisPheIleProAspAlaAs 245 638 TTCCTAACGAAAATATGTCTTTGAAAAAATAACAAATACTACGACTCA 687 245 nThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyProP 262 738 AACAGGGTATAAAATGTATGAAATGAAGAGCTAGAT......GCAA 778 779 TITITGGTTCC...ATACCCCCAGATCTAATCAAAATCTAAAATTAAGA 825 279 GlyHisLeuHisSerPheAspValAlaGlyThrSerTrpLeuThrPheAs 295 38 IleAsnIleArgAspGluProArgSerLeuAspProArgGlnValArgLe 262 roTrpGlyGluArgIleProGlnGluThrLeuSerAsnLeuGlnSerLys 505.50 Length: 485 1.620 Caps: 15 64.330 Percent Identity: 28.041 Align seg 1/1 to: AAX61763 from: 1 to: 1587 US-09-824-567-2 x AAX61763 alignment_scores: Quality: Percent Similarity: Ratio: 120 152

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Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NN1999.DAT:AAX20248
                                                                                                                                                                                                                        973 ACTACCCCTACAAGAAGAAGAACTCCCAACTTTAGTTCATAT...... 1014
1015 .....TCTTATGCAAAAAGTTTAGAAT 1036
                                                                                                                                                                                                                                                                                                                                                                            1037 TATTIAATCCTGAAAATTGCAAAAACCCTTCTAGCTGAAGCTGGATATCCT 1086
                                                  295 nIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaS 312
                                                                           | :::
| R76 TACACACATCAAACCACTTGACGTTAAAATTAGAAAGCCTTAACTC 925
                                                                                                                       312 erAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyArgAla 328
                                                                                                                                                    926 TIGCTAITGACAGAGAAACGCITACATATAAAGII...CTIGACAACGGG 972
                                                                                                                                                                                              329 LysThralaaspHisLeuLeuProThrAsnIleHisSerTyrProGluHi 345
                                                                                                                                                                                                                                                                      345 sGlnLysGlnGluMetAlaGlnArgGlnAlaTyrAlaLys.....LysL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1134 AGCAAATAAAAAATTTGTGAATTTATTCAAAACCAATGGAAAAAATT 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 rAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLysGluSerL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 euGlyPhealaileProileValGlyLysGluPheAlaLeuLeuGlnAla 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAs 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437 pPhealaAspProMetalaPheLeuThrIlePheAlaTyrProSerGlyV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454 alProProTyrAla.....IleAsnHisLysAspPheLeuGlulle 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 LeuGlnAsnIleGluGlnGlnGlnAspHisGlnLysArgSerGluLeuVa 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 lSerGlnAla...SerLeuTyrLeuGluThrPheHislleIleGluProI 500
                                                                                                                                                                                                                                                                                                                                           360 euPheLysGluAlaLeuGluGluLeuGlnIleThrAlaLysAspLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                     HisLeuAsnLeuIlePheProVal.....SerSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1328 ACACACAATTCTCATCATCATAATTACTCAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi polynucleotide sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAX20248 standard; DNA; 910715 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1478 TATAC 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 leTyr 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX20248;
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573740 TTAGAATTTTAAATAAAGAAACTGGCTCAAAGTACGTTGAAATGGTTAAA 573691
                                                                                                                        152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of binfections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 910715 BP; 327171 A; 129646 C; 130753 G; 323091 T; 54 other;
                                                                                                                                                                                                                                                                                                                                                                             New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573990 ATAAGCTTGGGAGCAGAGCAGCAGTCTTGACCCTCAATTAGCAGAGA 573941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573940 TAATGTCGCATCAAAAATGATTGACACAAGATGTTAGAGGATTGTTACAG 573891
                                                                                                                                                                                                                                                                                                       Smith HO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573890 GAGATCCTAATACAGGGGGAAATAAACCGGGACTTGCAAAAGGGTGGGAT 573841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573790 IIGGAGIGACGAGIIGCAATCACIGCAGAAGGAAIIAGAAAICIIAIC 573741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 LeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSerAlaPhe. 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 .TrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGluSerTrpL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 ysGlnValAlaThrGlnGluValSerGlyIleTyrAla...PheAlaLeu 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 IleAsnIleArgAspGluProArgSerLeuAspProArgGlnValArgLe 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 uLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeuValGlnG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 luAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAspTyrSer 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 910715
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Gaps: 15
Percent Identity: 28.041
                                                                                                                                                                                                                                                                                              Dougherty BA, Fraser C, Lathigra R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AAX20248 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 157-671; 1128pp; English.
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97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC. (MEDI-) MEDIMMUNE INC.
                                                                                                                         98WO-US12764.
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US-09-824-567-2 x AAX20248/rev
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64.330
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                Borrelia burgdorferi.
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Ratio:
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                                                                                                                                                                      20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                  WO9858943-A1
                                                                                                                      18-JUN-1998;
                                                                                  30-DEC-1998
                                                                                                                                                        03-SEP-1997;
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White OR;
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573640 TGAACTTGGAATTAGAGGGATTGATGAAAAACATTAGAAATAACACTGG 573591
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573590 AAICACCAAAACCTTATTTTATTGATATGTTAGTACACCAATCATTATT 573541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573396 AATGAAGTAGAATTAGAAGATTACATTTTACACAACAAATGACAGCTC 573347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573446 ITCCTAACGAAAATATGTCTTTGAAAAAATAACAAATACTACGACTCA 573397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                573346 AACAGCGTATAAAATGTATGAAAATGAAGAGCTAGAT......GCAA 573306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573305 TITITGGITCC...AIACCCCCAGAICTAAICAAAAAICTAAAAITAAGA 573259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573258 AGCGACTATTACTCATCAGCTGTTAATGCCATATACTTTTACGCGTTCAA 573209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                573208 TACACACAICAAACCACITGACATTAAAATTAGAAAGCCTTAACIC 573159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573069 .....TCTTATGCAAAAGTTTAGAAT 573048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573047 TATITAATCCIGAAATIGCAAAACCCTICTAGCIGAAGCIGGATATCCI 572998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572950 AGCAAATAAAAAATTTGTGAATTTTTTCAAAACCAATGGAAAAAAATT 572901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHisPheGlyValHisSerProAsnGluSerThrLeuValValThrLeuG 169
                                                                                                                                                                                                              169 luSerProThrSerHisPheLeuLysLeuLeuAla......Leu 181
                                                                                                                                                                                                                                                                                                                        182 ProvalPhePheProvalHisLysSerGlnArgThrLeuGlnSerLysSe 198
                                                                                                                                                                                                                                                                                                                                                                                                                                198 rLeuPro.....IleAlaSerGlyAlaPheTyrProLysAsnIleL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 ysGlnLysGlnTrpIleLysLeuSerLysAsnProHisTyrTyrAsnGln 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGlnValGluThrLysThrIleThrIleHisPheIleProAspAlaAs 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 nThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyProP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 roTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuGlnSerLys 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 GlyHisLeuHisSerPheAspValAlaGlyThrSerTrpLeuThrPheAs 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 nIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 eralaLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyArgAla 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 LysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyrProGluHi 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 sGlnLysGlnGluMetAlaGlnArgGlnAlaTyrAlaLys.....LysL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 euPheLysGluAlaLeuGluGluLeuGlnIleThrAlaLysAspLeuGlu 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 HisLeuAsnLeullePheProVal......SerSerSe 387
136 AsnProIleLysAsnValArgLysIleGlnGluGlyHisLeuSerIleAs
                                                                                                                                                                                                                                                                                                                                                                        573540 CCAGTA.....CCAGTICATGTTACCGAAAAGTAIGGACAAAACTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573158 TIGCTATTGACAGAGAGACGCTIACATATAAAGTT...CTTGACAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 rAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLysGluSerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 euGlyPheAlaIleProIleValGlyLysGluPheAlaLeuLeuGlnAla
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Sequence 1659 BP; 582 A; 305 C; 359 G; 413 T; 0 other;

activity.

SXS

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The present sequence represents a gene isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vectines for preventing or attenuating an infection caused used for detecting Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
detection; attenuation; antigenic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
                          572706 ATAAAGAAATCCGACCTTGAGCTTGATCCAATAAAAGAGAGAAGACATTTT 572657
                                                                                                                                                                                                                                                                                             572656 AAGACAAAGCAGAAGAGATAATTGAAAAAGATTTTCCAATAGCACACAA 572607
                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX20020
                                                                437 pPheAlaAspProMetAlaPheLeuThrIlePheAlaTyrProSerGlyV 454
                                                                                                                                 454 alProProTyrAla.....IleAsnHisLysAspPheLeuGlulle 467
421 AspleuSerSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAs 437
                                                                                                                                                                                                468 LeuGlnAsnIleGluGlnGlnGlnAspHisGlnLysArgSerGluLeuVa 484
                                                                                                                                                                 572756 ACACACAATTCTCATCTCATAATTACTCAAACCCAGAATACAACGAACTT
                                                                                                                                                                                                                                                                 484 lSerGlnAla ... SerLeuTyrLeuGluThrPheHisIleIleGluProl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis gene EF012.
                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAX20020 standard; DNA; 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-070095/06.
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16-MAY-1997;
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| GECCGCATGTGGCGGAACCAAAGAAGCGGCAGAGAAAGTAGATTCGGGAA 115
                                                                                                                                                                                                                                                                                                                                                                                                       116 ATTTAGCAGCTGAACAAAAATCAGTATTAGTTCACCTGCACCAATCTCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 ACATTGGATACAACAACAACAACAGATAAAAATACCTTTACAATGGCACA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 ..CCAGCTCTAGCTAAAGATGTCAAGATTAGTGACGATGGGCGCAAGTAC 312
                                                                                                                                                                                                  4 ileSerValGlyileCysIleThrIleLeuLeuSerLeuSerValValLe 20
                                                                                                                                                                                                                                  20 uGlnGlyCys......bysGluSerSerHisS 29
                                                                                                                                                                                                                                                                                                                                                                29 erSerThrSerArgGlyGluLeuAlalleAsnIleArgAspGluProArg 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 SerLeuAspProArgGlnValArgLeuLeuSerGluIleSerLeuValLy 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 ThrPheLysLeuLysSerAlaPhe...TrpSerAsnGlyAspProLeuTh 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 ralaGluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 TIGGACCGAATGCCTATTTACTAGACAGTGTTAAAATAGTTTTGAAATA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sHislleTyrGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 luProAlaLeuAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyr 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 erGlylleTyrAlaPheAlaLeuAsnProlleLysAsnValArgLysIle 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnGluGlyHisLeuSerIleAspHisPheGlyValHisSerProAsnGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 CGCAACGGTGAAAAGTCAGTCGATGAATTAGGGATTTCAGCCCCGAATGA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 uSerThrLeuValValThrLeuGluSerProThrSerHisPheLeuLysL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563 TCGTTTCGATTGCTTGGTTAGCGCCACAAAATCAAAATTTGTCGAAGCG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 CAAGGCAAAGAITACGCCTIGGATAGTGAACATTTACTTTATAGCGGGCC 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 aPheTyrProLysAsn.....IleLysGlnLysGlnTrpIleLysLeus 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....IleAlaSerGlyAl 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     663 ATTTACGCTAGCCAATTGGGATGCGACTTCAGATACTTGG...ACATTGA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 erLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrLysThrIle 236 ::|||||||||||:::|||||||::: :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euLeuAlaLeuProValPhePheProValHisLysSerGlnArgThrLeu
                                Length: 539
Gaps: 15
Percent Identity: 25.232
                                                                                                                                                                    from: 1 to: 1659
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                                            1.346 62.709
                                                                                                                                                            Align seg 1/1 to: AAX20020
                         455.00
                                                                                                                     US-09-824-567-2 x AAX20020
                                                       Percent Similarity:
                     Quality:
                                            Ratio:
alignment_scores
                                                                                                  alignment_block
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237 ThrileHisPheIleProAspAlaAsnThrAlaAlaLysLeuPheAsnGl 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710 AAAAAATCCAGAATACTATGATGCGGATCAAGTGAAACTGGAAGAAGTT 759
                                                                                                760 GCGGTTAGCACAATCAAAGAAGATAATACTGGGATTAACTTATATCAAGT 809
                                                                                                                                                 253 nGlyLysLeuAsnTrpGlnGlyProProTrpGlyGluArgIleProGlnG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1139 GGACGAAAGCCCAAGCGGATGTCGGTAAAAGTGAAACTTTCATTGCTG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1189 GCGGCAGACACAGATCAAGGAAAACGAATTGCTGAATATGTTCAAAGTCA 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 uAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1289 GTAATAATGTGAACCAATCGCGACGTGAAAAAATTATGAGTTGTCTCTT 1338
                                                                                                                                                                                                                                                                                                                                               286 ValAlaGlyThrSerTrpLeuThrPheAsnIleAsnLys...PheProLe 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 laLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisLeu 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 LeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGluMetAl 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1339 TCAGGATGGATTGCCGGCAGTAGTGAATTAGACTCTTACTTTAACTTATA 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 ProValSerSerAlaSerSerLeuLeuValGlnLeulleArgGluGl 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1389 IGCAGGAGAAICAAGITAC...AAITACGGCAAITAICAIAAIGCCAAAI 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1436 ACGACCAATTGGTAGAAGAGGCACGAACGATTAATGCCAATAATCCAGAG 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1486 AAACAGTIIGCAGAATACAAAGAGGGGAAGACAICTIGIIGAACCAAGA 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 nTrpLysGluSerLeu...GlyPheAlalleProlleValGlyLysGluP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 heAlaLeuLeuGlnAlaAspLeuSerGerGlyAsnPheSerLeuAlaThr 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 GlyGlyTrpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePh 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 GlnLysArgSerGluLeuValSerGlnAlaSerLeuTyrLeuGluThrPh 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 eHisIleIleGluProlleTyrHisAspAlaPheGlnPheAlaMetAsnL 511
                                                                                                                                                                                                810 GAAIGAACIAGACITA.....GITCGCAITAACGGAC
                                                                                                                                                                                                                                               270 luThrLeuSerAsnLeuGln...SerLysGlyHisLeuHisSerPheAsp
                                                                                                                                                                                                                                                                                              842 AATATGTTCAACAATATCAAGATCCAGGCTATGTCAGGTCATCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 aGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1039 ATTCCAAGTAAACTTTATGCGAATCCAGAAACGGATGAAGATTTCCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 euGlnIleThrAlaLysAspLeu...GluHisLeuAsnLeu...IlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 eAlaTyrProSerGlyValProProTyrAlaIleAsnHisLys......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463 .....AspPheLeuGlulleLeuGlnAsnIleGluGlnGluGlnAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1586 CTAAATTGAAAGGCATT 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    511 ysLysLeuSerAsnLeu 516
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98. nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with of Enterococcus faecalis namples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                 Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX13087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11739 BP; 3917 A; 2161 C; 2537 G; 3118 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2994 AIGAAATIGGGGAAAAAAAGTAGTTIGATIGCAACAGGGTITCITT 3043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 IleSerValGlyIleCysIleThrIleLeuLeuSerLeuSerValValLe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .. LysGluSerSerHisS 29
                                                                                                                                                  Enterococcus faecalis genome contig SEQ ID NO:150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 539
Gaps: 15
Percent Identity: 25.232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 11739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 862-868; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunsch CA;
                               seq_documentation_block:
ID AAX13087 standard; DNA; 11739 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                        97US-0044031.
                                                                                                                                                                                                                                                                                                                                       98WO-US08985
                                                                                                                                                                                                                                                                                                                                                                       97US-0066009
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.346
62.709
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                                                                                                                                                                                                                                   Enterococcus faecalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-045171/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 uGlnGlyCys..
                                                                                                                  19-MAR-1999
                                                                                                                                                                                                                                                                  WO9850555-A2
                                                                                                                                                                                                                                                                                                                                     04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                       L4-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                    12-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
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                                                                                  AAX13087;
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| 304 | ::: | |
|----------------|--|--|
| 3094 | erSerThrSerArgGlyGluLeuAlaIleAsnIleArgAspGluProArg | |
| 46 | SerLeuasperodrugalnvalargialiaGiTCACCTGCACCAATCTCA 314 ::: | |
| 62 | | |
| 79 | luProalaLeualaGluAspTyrSerLeuSerSerAspGlyLeuThrTyr 95 | |
| 96 3291 | , « | |
| 111 3341 | | |
| 128 3391 | | |
| 145 | | |
| 161 | | |
| 178 | | |
| 195 591 | 200 | |
| 205 | | |
| 220 | | |
| 237 7 | 25 | |
| 253 1 | | |
| 270] 320 Å | | |
| 886 V | | |
| 101 n | 318 | |

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Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic; ss.
9917 AGCGAATGTTCATTTACGAAAAGCGATTGGCCAAGCAATTGATAAAGAAG 3966
                                                               ### 4017 ATTCCAAGTAAACTTTATGCGAATGCAGAAAGGGATGAAGATTTCCGAGC 4066
                                                                                                                                                                                                                        4067 TTACAGTGGCGAATATTTGAAAAATGACGTCAAAAAAGCTCAAGCTGAAT 4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.baT:Aax20021
                                                                                                                                                                                                                                                                                             4117 GGACGAAAGCCGAAGCGGATGTCGGTAAAAAGTGAAACTTTCATTGCTG 4166
                                                                                                                                                                                                                                                                                                                                                                    | 167 GCGGCAGACACAGATCAAGGAAAACGAATTGCTGAATATGTTCAAAGTCA 4216
                                                                                                                                                                                                                                                                                                                                                                                                                                           4267 GTAATAATGTGAAACCAATGCGGACGTGAAAAAAATTATGAGTTGTCTCTT 4316
                                   318 laLeuValSerThrIlePheLeuGlyArgAlaLysThrAlaAspHisLeu 334
                                                                                                            335 LeuProThrAsnlleHisSerTyrProGluHisGlnLysGlnGluMetAl 351
                                                                                                                                                                                       aGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluL 368
                                                                                                                                                                                                                                                              368 euGlnIleThrAlaLysAspLeu...GluHisLeuAsnLeu...IlePhe 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::|||||||::|||||
4317 TCAGGAFGGATTQCCGGCAGTAGTGATTAGACTCTTACTTTAACTTATA 4366
                                                                                                                                                                                                                                                                                                                                       383 ProValSerSerSerAlaSerSerLeuLeuValGlnLeuIleArgGluGl 399
                                                                                                                                                                                                                                                                                                                                                                                                               399 nTrpLysGluSerLeu...GlyPheAlalleProlleValGlyLysGluP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4367 TGCAGGAGAATCAAGTTAC...AATTACGGCAATTATCATAATGCCAAAT 4413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4414 ACGACCAATTGGTAQAAGGCACGAACGATTAATGCCAATAATCCAGAG 4463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 heAlaLeuLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThr 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 GlyGlyTrpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePh 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4464 AAACAGTITGCAGAATACAAAGAAGCGGAAGACAICTTGTIGAACCAAGA 4513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 .....AspPheLeuGluIleLeuGlnAsnIleGluGlnGluGlnAspHis 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 GlnLysArgSerGluLeuValSerGlnAlaSerLeuTyrLeuGluThrPh 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 eHisIleIleGluProlleTyrHisAspAlaPheGlnPheAlaMetAsnL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 eAlaTyrProSerGlyValProProTyrAlalleAsnHisLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis EF012 gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAX20021 standard; DNA; 1585 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX20021;
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WO9850554-A2. 12-NOV-1998.

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The present sequence encodes an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. daecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nuclectide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1585 BP; 559 A; 296 C; 336 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                Hromockyj A, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 90-91; 301pp; English.
                                                                97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
   98WO-US08959.
                                                                                                                                                                                                                                                                        Bailey C, Choi GH,
                                                                                                                                                                                                                                                                                                                                         WPI; 1999-070095/06.
                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY00031
                                                                14-NOV-1997;
06-MAY-1997;
04-MAY-1998;
                                                                                                                                    16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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55 TGAACAAAAATCAGTATTAGTTCACCTGCACCAATCTCAACATTGGATA 104
                                                                                                                                                                                                                                                                                                                                                                                                   105 CAACACAAAAAAAAAAAAAAAAAAAAAAAGGCACAACATTATTT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGCCTTTATCGGTTTGATGATGATAGTGCCACGTG...CCAGCTCT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 euLysSerAlaPhe...TrpSerAsnGlyAspProLeuThrAlaGluAsp 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 TGCGGGAGGGATTAAGTGGAGCAACGGCGACCAATCACGGCCCAAGAT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 PhelleGluSerTrpLysGlnValAlaThrGlnGluValSerGlyIleTy 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 TITGITIATICITGGAAAAACTGGTGACACCAGGGACGATGGACCGAA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 rAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGlnGluGlyH 148
                                                                                                                                                                                  22 GlyCysLysGluSerSerHisSerSerThrSerArgGlyGluLeuAla.. 37
                                                                                                                                                                                                                       8 GGAACCAAAGAAGCGGCAGAGAAGTAGATTCG...GGAAATTTAGCAGC 54
                                                                                                                                                                                                                                                                      38 ......IleAsnIleArgAspGluPro.....ArgSerLeuAspP 49
                                                                                                                                                                                                                                                                                                                                                        49 roArgGlnValArgLeuLeuSerGluIleSerLeuValLySHisIleTyr 65
                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 uAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysL 99
    Length: 519
Gaps: 17
Percent Identity: 26.590
                                                                                                                                                from: 1 to: 1585
                    1.380
63.198
452.50
                                                                                                                                              to: AAX20021
                                                                         alignment_block:
US-09-824-567-2 x AAX20021
                    Ratio:
Percent Similarity:
Quality:
                                                                                                                                            Align seg 1/1
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148 isLeuSerIleAspHisPheGlyValHisSerProAsnGluSerThrLeu 164
                                                                                                                                                 165 ValValThrLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLe 181
                                                                                                                                                                                       452 ATTGTTGAATTAAAACAGGCCCAACCTTCCTTGTTAGCAGTCGTTTCGAT 501
                                                                                                                                                                                                                                     181 uProValPhePheProValHisLysSerGlnArgThrLeuGlnSerLysS 198
                                                                                                                                                                                                                                                                                                                         198 erLeuPro......IleAlaSerGlyAlaPheTyrPro 208
                                                                                                                                                                                                                                                                         602 GCCAATIGGGAIGCGACTICAGAIACTIGG...ACATIGAAAAAATCC 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 helleProAspAlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLysLeu 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 AsnTrpGlnGlyProProTrpGlyGluArgIleProGlnGluThrLeuSe 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 rAsnLeuGln...SerLysGlyHisLeuHisSerPheAspValAlaGlyT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      978 AACTITATGCGAATCCAGAAACGGATGAAGATTTCCGAGCTTACAGTGGC 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            028 GAATATITGAAAAATGACGTCAAAAAGGICAAGGIGAATGGACGAAAGC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTTA.....GTTCGCATTAACGGACAATATGTTCA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 ACAATATCAAGATGATCCAGGCTATGTCAGTCATCCAGATGTGGCC...A 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 hrSerTrpLeuThrPheAsnIleAsnLys...PheProLeuAsnAsnMet 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       828 ACTACTICITAGALTICAACAAAAAGAAGGAACGCCATTAGCGAATGTT 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 LysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLeuValSe 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rThrllePheLeuGlyArgAlaLysThrAlaAspHisLeuLeuProThrA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1128 CAGATCAAGGAAAACGAATTGCTGAATATGTTCAAAGTCAGTTGCAAGAA 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 AlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGlnIleTh 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             snileHisSerTyrProGluHisGlnLysGlnGluMetAlaGlnArgGln 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 rAlaLysAspLeu...GluHisLeuAsnLeu...IlePheProValSerS 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 erSerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLysGlu 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418 uGlnAlaAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyJrpP 435
                                                                                             :: :: 11111 111
552 ATTACGCCTIGGAIAGIGAACATITACITITAIAGGGGGCCATITACGCIA
                                                                                                                                                                                                                                                                                                                                                                                                          209 LysAsn.....IleLysGlnLysGlnTrpIleLysLeuSerLysAsnPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 oHisTyrTyrAsnGlnSerGlnValGluThrLysThrIleThrIleHisP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 SerLeu...GlyPheAlaIleProIleValGlyLysGluPheAlaLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338
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1228 GAACCAATCGCGACGTGAAAAAATTATGAGTTGTCTCTTTCAGGATGGA 1277

435

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to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                       Sequence 26811 BP; 8978 A; 3456 C; 3596 G; 10780 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14530 ATAAAAAAGTTAAAAAGTTGTATTATTTCTCAATTTAATTTTACTTATTTC 14481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14480 frgir......AATGAAAGIAATAGAAACAAAT 14452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14451 IGGTTTTAAGCTAAATATTGAAGTGAGCCTGCTACTTTAGATGCTCAA 14402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14351 CATTTTAGATGGAGATCCCAGGACTGGAGGATACAGACCGGGACTTGCTA 14302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14301 AAAGTTGGGATATTTCTGATGACGGAGTAGTTATACGTTTCATTAAAGA 14252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14251 GATAATCTTGTTTGGAGTGATTTCCATTACTGCCGAAGAATA.AG 14203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14202 AAAATCTTATCTTAGAATTTTAGATAAAGAAACCGGCTCATCTTTTGTTA 14153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14152 ACATGATTAAGTCCGTTATTAAAAATGCAGAAGAGTATTTTGACGGCAAA 14103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14102 GCAAATGAGTCTGGAGCTTGGAATTAAAGCTCTTGATGAAAAAACTTTAGA 14053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14052 AATAAGGCTAAAATCTCCAAAGCCATATTTTCTTGATATGTTAGTACATC 14003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: ||||
13952 TGGACAGACCCCGAGAATATGGTTGTTAGTGGTCCTTTCAAATTAAAATC 13903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetArgLyslleSerValGlyIleCyslleThrIleLeuLeuSerLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 rValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ...SerAlaPheTrpSerAsnGlyAspProLeuThrAlaGluAspPhe11 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 eGluSerTrpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 heAlaLeu...AsnProlleLysAsnValArgLysIleGlnGluGlyHis 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 yLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 LeuSerlleAspHisPheGlyValHisSerProAsnGluSerThrLeuVa 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 lValThrLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 roValPhePheProVal.....HisLysSerGlnArgThrLeuGlnSer 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 nIleLysGlnLysGlnTrpIleLysLeuSerLysAsnProHisTyrTyrA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14401 TTAATAAACGATACGGTTGGATCAGGGATTGTAAGCCAAATGTTTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 26811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 LysSerLeuPro......IleAlaSerGlyAlaPheTyrProLysAs
                                                                                                                                                                                                                                           Length: 501
Gaps: 15
Percent Identity: 26.347
                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: AAX20253
                                                                                                                                                                                                                                                                                                                                           US-09-824-567-2 x AAX20253/rev
                                                                                                                                                                                                                              451.50
1.360
66.267
                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
  828888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX20248 to AAX20402 represent polynuclectide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX20253
                                                      1278 TIGCCGGCAGTAGTGAATTAGACTCTTACTTTAACTTATATGCAGGAGAA 1327
                                                                                                                                                        1328 TCAAGTIAC...AATTACGGCAATTATCATAATGCCAAATACGACCAATT 1374
                                                                                                                                                                                                                                                     1375 GGTAGAAGAGGCACGAACGATTAATGCCAATAATCCAGAGAAAACAGTTTG 1424
                                                                                                                                                                                                                                                                                                                                                     1425 CAGAATACAAAGAGAGGAAGACATCTTGTTGAACCAAGATGCTGCCCAA 1474
          heAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyrPro 451
                                                                                                                                                                                                                                                                                                                                                                                                                                     452 SerGlyValProProTyrAlaIleAsnHisLys......AspPh 464
                                                                                                                                                                                                                                                                                                    481 erGluLeuValSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIle 497
                                                                                                                                                                                                                                                                                                                                                                                                      498 GluprolleTyrHisAspAlaPheGlnPheAlaMetAsnLysLeuSe 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HÖ;
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                                                                                                                                                                                                    464 eLeuGluIleLeuGlnAsnIleGluGluGluGluGlnAspHisGlnLysArgS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clayton R, Dougherty BA, Fraser C, Lathigra R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi polynucleotide sequence #6.
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seq_documentation_block:
ID AAX20253 standard; DNA; 26811 BP.

04-MAY-1999 (first entry)

AAX20253;

Claim 1; Page 851-867; 1128pp; English.

97US-0057483, 97US-0050359, 97US-0053344,

20-JUN-1997; 03-SEP-1997;

22-JUL-1997;

97US-0053377

98WO-US12764.

18-JUN-1998;

30-DEC-1998

Borrelia burgdorferi.

WO9858943-A1

(HUMA-) HUMAN GENOME SCI INC.

(MEDI-) MEDIMMUNE INC.

WPI; 1999-081217/07.

White OR;

AAX13139;

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13805 AATAGCATTACAGCTTATAATATGTAT......tTAAATGATGA 13768
                                                                                                                                                                                                                                       13767 GCTGGATGCAATTTTTAAGAATGTTCCACCAGATTTGCTTAAGGATCTTA 13718
                                                                                                                                                                                                                                                                                                                                13717 AGCTTAGGGACGATTATTATTCAATGGGTATTAATTCAACCTCTTTTTAT 13668
                                                                                                                                                                                                                                                                                                                                                                                                                                13667 TCTTTGAACATGAAAGTAAAACCGCTTGACAATGTTAAAGTTAGAAAGGC 13618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...AATGATAGTTCTATTCCTACAAGA...AGAGCAACT 13539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13488 IGAAATGGCAAAGAAGCTTTTGGCAGATGCAGGATATCCC.....A 13448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: ::::::!!
13397 CAGAGAAAA...ATTGCTGAATTTATTCAAAATCAGTGGAAGAAAAACTT 13351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13350 AAATATTAATGTACAGCTTGAGAATGAAGAATGGTCAACATATATAAATA 13301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 snGlnSerGlnValGluThrLysThrIleThrIleHisPheIleProAsp 243
                                                                                                                                                                                         259 nGlyProProTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13200 TITITCAICTIAIGGATAITCAAATICTGAATAIGATGAACTITAATAA 13151
                                                                                                                                                                                                                                                                                    276 lnSerLysGlyHisLeuHisSerPheAspValAlaGlyThrSerTrpLeu 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13150 AATCAGATAATGAGAGAGATATTTTAAAAGACAGGAAATTCTAAAAAA 13101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 aLeuAlaSerAlaLeuAspLysGluAlaLeuValSerThrIlePheLeuG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 lyArgAlaLysThrAlaAspHisLeuLeuProThrAsnIleHisSerTyr 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 a...TyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGlnIleT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 hrAlaLysAspLeuGluHisLeuAsnLeuIlePheProValSerSerSer 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 AlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLysGluSerLe 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 uGlyPhealaIleProlleValGlyLysGluPheAlaLeuLeuGlnAlaA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 spleuSerSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAsp 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 PheAlaAspProMetAlaPheLeuThrIlePhe...AlaTyrProSerGl 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 yValProProTyrAlaIleAsnHisLysAspPheLeuGluIleLeuGlnA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 snIleGluGlnGluGlnAspHisGlnLysArgSerGluLeuValSerGln 486
                                                                                              244 AlaAsn...ThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13538 CCAGATTATATTGATTACTCTTATAAAAGCAATTTGAGCTTATTGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 ProGluHis.....GlnLysGlnGluMetAlaGlnArgGlnAl
                                                                                                                                                                                                                                                                                                                                                                                   293 ThrPheAsnIleAsnLysPheProLeuAsnAsnMetLysLeuArgGluAl
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seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX13139 seq_documentation_block: ID AAX13139 standard; DNA; 10996 BP.

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New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                    Enterococcus faecalis; contig; detection; Enterococcal infection;
                                                              vaccine; attenuation; computer readable medium; ds
                                     Enterococcus faecalis genome contig SEQ ID NO:202.
                                                                                                                                                                                             CA;
                                                                                                                                                                                             Kunsch
                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                             98WO-US08985
                                                                                                                                            6009900-Sn26
                                                                                                                                                            97US-0046655
                      19-MAR-1999 (first entry)
                                                                                                                                                                                          Dillon PJ,
                                                                             Enterococcus faecalis
                                                                                                                                                                                                        WPI; 1999-045171/04.
                                                                                                                                          14-NOV-1997;
                                                                                            WO9850555-A2
                                                                                                                            04 - MAY - 1998;
                                                                                                                                                          6-MAY-1997;
                                                                                                            L2-NOV-1998
                                                                                                                                                   06-MAY-1997
                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                  infection.
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX1293 to AAX1293 perseent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence diagnosing Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences infection.

Claim 1; Page 1065-1071; 2084pp; English.

Sequence 10996 BP; 3633 A; 1848 C; 2288 G; 3223 T; 4 other;

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51 TGCAGATTTATCTTTAGGAACAGATACAATTAGTTTTACGGCACTGAATA 100
                                                                                                                                                                                                                     30 SerThrSerArgGlyGluLeuAlaIleAsnIleArgAspGluProArgSe 46
                                                                                                                                                                                                                                                                 1 ACTGCCGCTAAACAAGAATTTAAAGTAGTAGTTCAACAAGAAATGCCTTC 50
                                                                                                                                                                                                                                                                                                               46 rLeuAspProArgGlnValArgLeuLeuSerGluIleSerLeuValLysH 63
                                                                                                                                                                                                                                                                                                                                                                                                    63 isIleTyrGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGlu 79
                           Length: 526
Gaps: 13
Percent Identity: 26.046
                                                                                                                                                                            Align seg 1/1 to: AAX13139 from: 1 to: 10996
                                           1.443
                         443.00
                                                                                                                            US-09-824-567-2 x AAX13139
                                                           Percent Similarity:
                         Quality:
                                         Ratio:
alignment_scores:
                                                                                                         alignment_block:
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| | 11 | 300 | 14 | 16 | 7 | TLeuGl 195 ::::: GTAGA 494 | aSerG 204 ::: TAATG 544 | 21 | GluTh 233 ::: AAATT 641 | aLysL 250 ::: GAACT 691 | 26 | 28. | =AsnL 298 :::: TAAAA 823 | laLeu 314 ::: GATT 873 | 'sThrAl 331 ::: 'AGTCGC 923 | 34 | rala 357 |
|--|---|--|--|--|--|--|---|--|--|--|---|--|--|--|--|--|---|
| erAspGlyLeuTh :: ATGATGGTCTGAC | AsnGlyAspProL | lAlaThrGlnGlu:::: | ysAsnValArgLy: :: \AAACGGTGCAGA(| /alHisSerProa ::: \TTAAAGCAAACG | SerHisPheLeul ::: .CCATATTTTGATT | ysSerGlnArgThrLeuGl ::::: | erLysSerLeuProlleAl :::::: CAGTGAAAAGCAGTCTA | GGCTCAGATACCA | nGlnSerGlnVal ::::::: TAAAGACAATGTC | laAsnThrAlaAl | ProProTrpGlyGluArg | rLysGlyHisLeu! ::: 3GATCCAGAATTGG | neAsnlle TAATCAGCGAGA1 | NaLeuAlaSerA ::::::: CAATTTCAGCAGC | GlyArgAlaLys1 ::: GACGCTCAGTAG | ProThrAsnlleHi ::: CGCCGACAGATGACAC | lnArgGlnAlaTy |
| TyrSerLeusers ::::: :: GTGCAAGTCAGTG | ralaPheTrpSer | PrTrpLysGlnVa. | euAsnProlleLy ::: : !TAGAAATGATTGI | AspHisPheGlyV :::::::: : :TCTGAATTAGGC | uGluSerProThr ::: GGCAAAACCAACA | heProvalHisLy CCCGCAACAL | SerLyss :::: | nIleLys ::::: CTTTGAAGGGGCT | roHisTyrTyrAs :::: :::: AAAACTATTGGGA | PhelleProAspA ::: ::: STTGTCAAGGAGG | AsnTrpGlnGly ::: AGAC | erAsnLeuGlnSea ::::::::: GCAAATGGCGAA | erTrpLeuThrP ::: GCTATTTGGAATT | LysLeuArgGluA ::: ::: :AATTTACGCAAAG | rThrIlePheLeu : ::: TAAAATTTTAGGO | GGATGTCGTATTC | GlnGluMetAlaG ::: AAAATTGTTGAAT |
| ProAlaLeuAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyrTh ::: | rPheLysLeulysSeralaPheTrpSerasnGlyaspbroLeuthra | laGluAspPheileGluSerTrpLysGlnValAlaThrGlnGluValSer | GlylleTyrAlaPheAlaLeuAsnProlleLysAsnValArgLyslleGl ::: :: ::: :: GCTGAGTATGCTTATTTTCTAGAAATGATTGAAACGGTGCAGACATTGT | nGluGlyHisLeuSerIleAspHisPheGlyValHisSerProAsnGluS | erThrLeuvalvalThrLeuGluSerProThrSerHisPheLeuLysLeu | LeualaLeuProvalPhePheProvalHisLy: ::: | n | 1yalapheTyrProLysasnileLysGlnLysGlnTrl | eLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluTh | rLysThrIleThrIleHisPheIleProAspAlaAsnThrAlaAlaLysL | euPheAsnGlnGlyLysLeuAsnTrpGlnGlyProProTrpGlyGluArg ::::: :: TATTCCAAGATGGCCAGGCAGAC | IleProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSe | rPheAspValAlaGlyThrSerTrpLeuThrPheAsnIleAsnL | ysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeu :: :::: | AspLysGluAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrA :::::: :: GATCGCAACGCATTAGTAGATAAATTTTAGGCGACGGCTCAGTAGTCG | aAspHisLeuLeuProThrAsnlleHisS | erTyrProGluHisGlnLysGlnGluMetAlaGlnArgClnAlaTyrAl :::: ::::::::: ::: ATTTGCTGATGAAAAAAAATTGTTGAATATAGCCCACAAAAA |
| 80 ProAl :: 151 GCAGG | 96 rPheL 1 201 AGTGA | 12 | 29 | 45 | 62 erThri 01 ACGAGC | 79 LeuAla 51 CTGGCC | 95 n : 95 GAAATA | er ω | 7 11 5 | 7 3 | 0 7 | | 8 4 | | 5 AspLysG :::: 4 GATCGCA | 1 aAsphis 4 TACCGGC | |
| 1 -1 | (7 | 17 | H 6 | 3 1 | 1 % | ∺ 4 | 19 | 20. | 21 59 | 23 | 25 69 | 267 724 | 283 | 298 824 | 31: | 331 | 341 |

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mar regulated polypeptide; NIMR; microbial infection; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS46237
                                1024 AAAGAATATIGGGCAAAAGGGAAGAAAGAATTGGGCATAACAACACTCAA 1073
                                                                                                       .074 AAIGGAI......AIIGIIGCCGAIGAIGICGAIICIACGAAAA 1111
                                                                                                                                                                             1112 AGTIAGCGGAAIATATTCAAGGTACGTIAAAGGAIACTITAGAGGCATT 1161
                                                                                                                                                                                                                                               1162 GATGTAACAGTGAGCCCAGTGCCGTTTTCAGTTCGAATTGATCGAGGTAG 1211
                                                                                                                                                                                                                                                                                                                 ||||| :::|||||| :::||||||| :::|||||:::
|1262 ATCCCAGTAGTTICTTAGAICTTITIGTTACIGGTAATAACTATAAICGC 1311
358 LysLysLeuPheLysGluAlaLeuGluGluLeuGlnIleThrAlaLysAs 374
                                                                     374 pLeuGluHisLeuAsnLeuIlePheProValSerSerSerAlaSerSerL 391
                                                                                                                                           391 euLeuValGlnLeuIleArgGluGlnTrpLysGluSerLeu...GlyPhe 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1312 GGGCGTTTTTCAAGTAAAGCCTACGATGAGTTGATTGAGGCTTCAGCTAC 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407 AlaileProileValGlyLysGluPheAlaLeuLeuGlnAlaAspLeuSe 423
                                                                                                                                                                                                                                                                                       423 rSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAlaAspPheAlaA 440
                                                                                                                                                                                                                                                                                                                                                           440 spProMetalaPheLeuThrIlePheAlaTyrProSerGlyValProPro 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1412 AGAAGITATIGATIGGIGAAGAGACCGCTITAGCACCACTITATCAAAG 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1462 GCGACTGCCCATCTACGCAGTAAAGAAGTGAAAGGCGTCGTTGCCCATGG 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                 457 TyralaileAsnHisLysAspPheLeuGluileLeuGln.....Asnil 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 eGluGlnGluGlnAspHisGlnLysArg...SerGluLeuValSerGlnA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 laSerLeuTyrLeuGluThrPheHisIleIleGluProIleTyrHisAsp 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                504 AlaPheGlnPheAlaMetAsnLysLysLeuSerAsnLeuGlyValSerPr 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel mar regulated protein (NIMR) #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1512 TGCTGGCGCACAATATGATTATAAGTGG 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 oThrGlyVal...ValAspPheArgTyr 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levy SB, Barbosa TM, Alekshun MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAS46237 standard; DNA; 12790 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-2000; 2000US-188362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TUFT ) TUFTS COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200170776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS46237;
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WPI; 2001-602769/68.

us-09-824-567-2.rng

Page 19

P-PSDB; AAU29335.

Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound -

Disclosure; Page 170-177; 526pp; English.

The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIMR nucleic acids and polypeptides are used in the treatment expression and activity. These modulators can be used to reduce the expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAS46278 represent Escherichia coli NIMR coding sequences of the invention.

Sequence 12790 BP; 3387 A; 3116 C; 3135 G; 3152 T; 0 other;

Length: 515 Gaps: 12 Percent Identity: 26.019 438.50 1.410 60.388 US-09-824-567-2 x AAS46237 Quality:
Ratio:
Percent Similarity: alignment_scores: alignment_block:

to: 12790 Align seg 1/1 to: AAS46237 from: 1 4 IleSerValGlyIleCysIleThrIleLeuLeuSerLeuSerValValLe 20

1391 TGCTGCAGAAGTTCCCGAGCGCCACAGTACTGGCAGAGAAGCAGGAGCTGG 1440

37 lalleAsnIleArgAspGluProArgSerLeuAspProArgGlnValArg

54 LeuLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeuYalGl 70

70 nGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAspTyrS 87

erLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLys...SerAla 102 87

103 PheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGluSerTr 119

151 IleAspHisPheGlyValHisSerProAsnGluSerThrLeuValValTh 167

1835 GCTTGATAAACCGTTGCCGTGGTTTGTGAATTTAACCGCTAACTTTGCCT 1884 1935 CCCGGAAATCTGATCGGCAATGGCGCTTATGTTCTTAAAGAGGGGGGTAGT 1984 167 rLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValP 184 213 nLysGlnTrplleLysLeuSerLysAsnProHisTyrTyrAsnGlnSerG 230 1985 CAATGAAAACTGGTCGTGGTACCGAATACCCATTATTGGGATAACGCCA 2034 2035 AAACGGTACTGCAAAAAGTGACCTTCCTGCCAATTAATCAGGAATCCGCA 2084 2118ATCACCGAATCCTTCCCGAAAATATGTATCAGAAGCTGT 2157 230 lnValGluThrLysThrIleThrIleHisPheIleProAspAlaAsnThr 246 2158 TGAAGGATATTCCGGGGCAGGTTTATACGCCGCCGCCGCAGCTCGGGACCTAT 2207 247 AlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyProProTr 263 263 pGlyGluArgIleProGlnGluThrLeuSerAsnLeuGlnSerLys.... 278 2208 TATTATGCGTTTAACACGCAAAAAGGGCCGACGGCAGATCAGCGCGTTCG 2257 1358 GGATTTACGCCGGAACCTTCGCCGTTTGAACAAAGGAGCAGGAAGA 2407 2496 AACCATCAAAAATTGCGATT...GCTGTAGCATCGATGTGGAAAAAGAA 2542 gGluAlaLeuAlaSerAlaLeuAspLysGluAlaLeuValSerThrilep 324 324 heLeuGlyArgAlaLysThrAlaAspHisLeuLeuProThrAsnIleHis 340AlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGlnI 370 2458 AACCGCTGAAG......CTGACGCTTTTGTATAACACTTCAGAA 2495 2543 CCTIGGCGTAGATGTTAAATTGCAAAATCAGGAATGGAAAACCTATATCG 2592 370 leThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProValSerSer 386 SerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLysGluSe 403 403 rLeuGlyPheAlaIleProIleValGlyLysGluPheAlaLeuLeuGlnA 420 420 laAspLeuSerSerGlyAsnPheSerLeuAlaThrGlyGlyTrpPheAla 436 453 yValProProTyrAlaIleAsnHisLysAspPheLeuGluIleLeuGlnA 470 SerGlnArgThrLeuGlnSer 1885 TCTTCCCGGTGCAAAAGCCAACGTAGAAAGCGGTAAAGAGTGGACGAAA LysSerLeuProlleAlaSerGlyAlaPheTyrProLysAsnIleLysGl 2085 GCCACTAAGCGTTACCTCGCGGGGATATTGAT..... 279GlyHisLeuHisSerPheAspValAlaGlyThrSer 291 TrpLeuThrPheAsnIleAsnLysPheProLeuAsnAsnMetLysLeuAr SerTyr...ProGluHisGlnLys...GlnGluMetAlaGlnArgGln.. 2408 GAATGCGCAGGCAAAAACTTTGTTGAGCGCAGCTGGTTATGGTCCGCAAA 437 AspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyrProSerGl hePheProValHisLys. 184 197 307 341 387

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The present sequence is the genome sequence of Listeria monocytogenes

Descriptions and primers for detecting sense in L. monocytogenes and related organisms, and primers for detecting genes in L. monocytogenes and Primers for detecting genes in L. monocytogenes and C. related organisms, and to study genetic polymorphisms and other genomes. The second for raising specific antibodies, identification of L. monocytogenes and related organisms, and for lossynthesis and L. monocytogenes and related organisms, and for Liosynthesis and C. biodegradation, especially biosynthesis of Vitamin B12. This sequence and C. requiate gene expression and cell replication and modulate in monocytogenes related diseases. In addition, this sequence and proteins concorded by it are useful in pharmaceutical and vaccines compositions for corransisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dehoux P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Durant L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Chakraborty T, Domann E, Hain T, Perche P, Charbit A, Durant L; Perche J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Domann E, Barla T, Reche P, Charbit A, Durant L; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listeria monocytogenes, useful e.g. for tree and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:ABA03041
:::::::||| :
2693 AGGAAATATTCACGCTTTAACAATCCGGCATATGACAAAGTTCTGGCC 2742
                                                                                                                                                          2743 AGGCAICGACGGAAAAIACCGTIAAAGCGCGTAAIGCCGAITACAACGCG 2792
                                                                                               470 snileGluGlnGluGlnAspHisGlnLysArgSerGluLeuValSerGln 486
                                                                                                                                                                                                                                                                               2793 GCAGAAAAATCCTCATGGAGCAAGCACCGATTGCACCAATTAT 2837
                                                                                                                                                                                                                        487 AlaSerLeuTyrLeuGluThrPheHisIleIleGluProlleTyr 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; gene therapy; vaccine; biosynth
vitamin B12; bacterial infection; disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes EGD-e genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID ABA03041 standard; DNA; 2944528 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 1; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2000; 2000FR-0004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchrieser C, Frangeul L, Dussurget O, Chetouani F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA03041;
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2286215GTGAAAAAATCTAAATTATTCTTACACTTGGATTAACACTATTACTAAG 2286166

17 rValValLeuGlnGlyCys....

1 MetArglysileSerValGlyIleCysileThrileLeuLeuSerLeuSe 17

Align seg 1/1 to reverse of: ABA03041

US-09-824-567-2 x ABA03041/rev

alignment_block;

from: 1 to: 2944528

Length: 579 Gaps: 20 Percent Identity: 25.043

470.50 1.368 59.413

Ratio:

alignment_scores: Quality: Percent Similarity: 2286115AAGGCTCAGATTCAGGAAAAGCTTCAGGAGAGCAAGTACTTAACTTGACA 2286066

25 luSerSerHisSerSerThrSerArgGlyGluLeuAlalleAsnIleArg

2286065GAAAAGCGCACTAATTCCTTCTGCAGACAGCACAAAAGCGGATGACCAAGT 2286016

42 AspGluPro....ArgSerLeuAspProArgGlnValArgLeuLeuSe

56 rGluileSerLeuValLysHisIleTyrGluGlyLeuValGlnGluAsnA 73

2286015TGGTTTGAACGTTGTAAACCAAACAAAGGTGTTATATGCG......

2285972..CTTGACAAAGATGGTATTCCTGCCATTGCCGGTGCTGCTGAAGAGCCA 2285925

73 snLeuSerGlyAsnIleGluProAlaLeu......AlaGluAspTyr 86

87 SerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLys...SerAl

102 aPheTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGluSerT

2285824GGCGTCGTGCAGTTGACCCTAACACTGCAACATATTCTTACCTATTT 2285775

119 rpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheAlaLeu 135

2285774GATGCAATCAAAAACGGTGGAGATATCGTAGCTGGCAAGAAAAAACCTGA 2285725

136 AsnProlleLysAsnValArgLysIleGlnGluGlyHisLeuSerIleAs 152

2285724AGAATTAGGAATTAAAQCAGTAGATGATTATACTTTAGAAGTTACTCTTT 2285675 2285674CTAAACCAACTGCTTACATTAACTCACTATTCGCATTCCCAACTTTCTTC 2285625 2285624CCACTIAACGAAAATTCGTTACGGAAAAAGGCCAAAAATATGCACAAAA 2285575 2285574TAGTGATAACATGTTATTCAATGGACCTTTCGAGTTGAAAGATTGGACTG 2285525 2285524GAACAAACAAAAAATGGACTTACGTA...AAAATGATAAATTGGGAT 2285478 152 pHisPheGlyValHisSerProAsnGluSerThrLeuValValThrLeuG 169 169 luSerProThrSerHisPheLeuLysLeuLeuAlaLeuProValPhePhe 185 186 ProValHisLysSerGlnArgThrLeuglnSe 196 196 rLysSerLeuProlleAlaSerGlyAlaPheTyrProLysAsnlle.... 211 228 GlnSerGlnValGluThrLysThrIleThrIleHisPheIleProAspAl 244 212 ..LysGlnLysGlnTrpIleLysLeuSerLysAsnPrOHisTyrTyrAsn Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;

ftp.wipo.int/pub/published_pct_sequences.

2284646CTTTATCAACGTTCTACTGCATACCTACAAAAAGACTACATTAAAAAGT 2284597 516 uGlyValSerProThrGlyValValAspPheArgTyr 528
2284596GCAAAAAAAATCCATTTGGT...CCAGATTACACTTAC 2284563

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                        OM protein - protein search, using sw model
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Run on:

July 26, 2002, 04:36:22; Search time 87.81 Seconds (without alignments) 1048.096 Million cell updates/sec

US-09-824-567-2 2739 Title: Perfect score:

1 MEKISVGICITILLSLSVVL......LSNLGVSPTGVVDFRYAKEN 532 Sequence:

Scoring table:

562222 seqs, 172994929 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_organelle:* sp_bacteria:* Sp_plant:*
sp_rodent:* SPTREMBL_19;* Sp_fungi:*
Sp_human:* sp_mamma]:* sp_virus:* sp_phage:* sp_mhc:* 10: 111: 12: 14: 15: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp_rvirus:

sp_archeap:

Q92899 chlamydia p Q84201 chlamydia t Q9pkj4 chlamydia m O92898 chlamydia p Q92896 chlamydia p Q9244 chlamydia p Q99446 chlamydia m Q97446 chlamydia m Q9745 obranja ag Q9765 obranja ag Q9559 borrelia ag Q98559 borrelia ag 054584 borrelia bu 0928y7 chlamydia p 09akr0 rhizobium m 0929h6 listeria in Description SUMMARIES Q9K244 Q9PKL9 Q84178 Q97D46 Q9K5F7 Q9PKJ4 Q928Y8 Q928Y6 Q928Y7 Q9AKR0 Q929H6 Q928Y9 084201 054584 Q9K5J9 031305 116 116 116 116 116 116 Query Match Length DB 4499.8 4497.4 4497.6 499.6 1199.6 118.5 117.6 117.5 100.0 2739 1364 1160.5 755.5 755.5 755.5 755.5 755.5 755.5 755.5 755.5 748 506.5 506.5 506.5 506.5 506.5 748.5 748.5 748.5 748.5 749 Score Result Š.

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|--------------|-----------------|----------|--------------------|--|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|---------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----|-----------|------|--------------------|-------------------|----------|-----|--------------|--------------------|--------------|--------------------|--------------------|
| 550 2 0930HR | 8 | 16 | | 2 | . 4 | 553 16 092784 | . 7 | 565 16 0971/18 | | 10 | 16 | 2 | ٥. | 4 | 1 - | ٦ ، | v , | 7 | 16 | 16 | 7 | 16 | 16 | 2 | 2 6 | 541 2 031304 | 4 - | 545 2 OF1642 | 4 . C | V |
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| 17 | | 19 | | | 22 | | 24 | 25 | 26 | | 28 | | | | | | | | 000 | | 4 | 4 | 30 | 40 | | 42 4 | | | 4.5 | • |

ALIGNMENTS

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MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia SECUENCE FROM N.A.
STRAIN=CML029;
MEDLINE-99206606; PubMed=10192388;
Malan S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999). MEDLINE-20330349; PubMed=10871362; Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chiamydia pneumoniae J138 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLRel. 19, Last annotation update)
01-DEC-2001 (TREMBLREL)
01-DEC-2001 (TREMBLR)
02-201 (TREMBLR)
02-201 (TREMBLR)
02-201 (TREMBLR)
03-201 532 AA. Nucleic Acids Res. 28:1397-1406(2000). PRELIMINARY; SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-AR39; STRAIN-J138 0928Y9 RESULT Q928Y9 ACCOOR OF THE STATE OF THE STAT

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NCBI_TaxID=83560;
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                                                                                                                                                                                                                                                                     61 VKHIYEGLVOENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWK 120
                                                                                                                                                                                                                                                                                                     121 QVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLA 180
                                                                                                                                                                                                                                                                                                                     181 LEVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHF 240
                                                                                                                                                                                                                                                                                                                                                                     241 IPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 LNNWKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 FKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLSSGNFSLATGGWFADFADFMAFLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISL 60
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                      481 SELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFRYAKEN 532
                                                                                                               59744 MW; 1CB473D9D46A1579 CRC64;
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01-NO-1998 (TrEMBLrel. 08, Last sequence update)
01-NOY-1998 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0LIGOPEPTIDE BINDING PROTEIN.
0PPA_3 OR CT198.
Chlamydia trachomatis.
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_TaxID=813;
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28.2311-2314(2000).
EMBL; AE001606; AAD18348.1; -
EMBL, AE002216; AAR38391.1; -
EMBL; AP002545; BAA98405.1; -
TIGR; CP0572; -
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MEDLINE=99000809; PubMed=9784136;
                                                                         InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
Complete proteome.
SEQUENCE 532 AA, 59744 MW; 1
                                                                                                                                                                Best Local Similarity 100. Matches 532; Conservative
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SEQUENCE FROM N.A.
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EISLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFI 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 RSWNDVLQNRVASIYSFAFLPI-DVNK------DSGFFAKDDHTLVINLLTPTPHFL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 KLLALPVEFPVH-KSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 ITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFN 295
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 INKEPLINIMKLREALASALDKEALVSTIFLGRAKTADHLLPINIHSYPEHQKQEMAQRQA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 TAKKPFSHSKLRQALSLVLNKEALASLAFV---KPAKHLLPAHLHTYPEQPSYKQQEAIT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Mite O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                      1 MRKISVGICITILLSLSVVLQGCKESSHSSTSRG----ELAINIRDEPRSLDPRQVRLLS 56
                                                                                                                                                                                                                                                                                                                                      356 YAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 ALLQADLSSGNFSLATGGWFADFADPMAFLTIFAXPSGVPPYAINHKDFLEILQNIEQEQ 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 518;
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01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PEPTIDE ABC TRANSPORTER, PERIPLASMIC PEPTIDE-BINDING PROTEIN,
                                                                                                                                                                                                                                                                 97; Mismatches 147; Indels
Chlamydia trachomatis.";
Science 28:754-759(1998).
EMBL: AE001293; AAC67790.1; -.
EMBL: PR000291; ABC-50.1; -.
Pfam; PF00496; SBP_bac_5.
Complete proteome.
SEQUENCE 518 AA; 58858 MW; 8B3AE840831BBEF1 CRC64;
                                                                                                                                                                                                                   49.8%; Score 1364; DB 16; 50.1%; Pred. No. 9.8e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydiales; Chlamydiaceae; Chlamydia.
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STRAIN=MOPN / NIGG;
MEDLINE-20150255; PubMed=10684935;
                                                                                                                                                                                                            Query Match
Best Local Similarity 50.1%
Matches 269; Conservative
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56 SEISLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDF 115
                                                                                                                                                                                                                                                                               116 IESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHF 175
                                                                                                                                                                                                                                                                                                       117 VRSWNDVLQNRIASIXSFAFLPI------DLSKD-CGFFAKDNHTLVINLHTPTPHF 166
                                                                                                                                                                                                                                                                                                                                  LKLLALPVFPPVH-KSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETK 234
                                                                                                                                                                                                                                                                                                                                                 TITIHPIPDANTAAKLENOGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLFF 294
                                                                                                                                                                                                                                                                                                                                                                                                    24; Gaps
                                                                                                                                                                             1 MRKISVGICITILLSLSVVLQGCKESS----HSSTSRGELAINIRDEPRSLDPRQVRLL 55
                                                                                                                                                                                             295 NINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPINIHSYPEHQKQEMAQRQ 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 ILAKTLLQBALTDLNNTIKDLEKCPLIFSATSSVNSQNAQWARDQWRRDGHTFFIGKEFIGSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415 FALLOADLSSGNFSLATGGWFADFADPMAFLTIFAYPSGVPPYAINHKDFLEILQNIEQE 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 QDHQKRSELVSQASLXLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFRYAKEN 532
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                                                                                                                            49.1%: Score 1345; DB 16; Length 520;
49.4%; Pred. No. 2.6e-92;
tive 103; Mismatches 145; Indels 24
                                                                                       520 AA; 59116 MW; 93E9C106CC0C7F58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0LIGOPEPTIDE BINDING PROFEIN.
0PPA_2 OR CPN0196 OR CP0571.
 Pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL, AE002315; AAF39319.1; --
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                                                                                                                        Query Match
Best Local Similarity 49.48; Pre
Matches 266; Conservative 103;
                                                   InterPro, IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
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SEQUENCE FROM N.A.
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                         Rad T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Bisen J., Fraser C.M.; DeBoy R., Kolonay J., McClarty G., Salzberg S.L., "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 NGEIKPALAESYTISEDGTRYTFKIKNILWSNGDFLTAQDFVSSWKEILKEDASSVYLKA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 LNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRTL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 QS--KSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAAKLFN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 QGKLINWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALAS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 HKKLDWGGPPWGEPIPPEISASLHQDDQLFSLPGASTTWLLFNIQKKPWNNAKLRKALSL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 ALDKEALVSTIFLGRAKTADHLLPTNIH--SYPEHQKQEMAQRQAYAKKIFKEALEELQI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 TAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLA 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 43.2%; Pred. No. 1.7e-78; 225; Conservative 111; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                           527 AA; 61166 MW; 628F32FB4F13D79E CRC64;
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43.2%; Pred. No. 1.7e
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STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
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Pfam; PF00496; SBP_bac_5; 1.
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EMBL; AE002215; AAF38390.1;
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SEQUENCE 527 AA.
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                                                                                                                                                                  STRAIN=J138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 ALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEEL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 LLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQEN 72
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                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CWL029;
MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-2030349; PubMed=10871362; Shirai M., Kishi F., Ouchi K., Shirai M., Hitakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Ouchi K., "Comparison of whole genome sequences of Chlamydia pneumoniae J138 Irom Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
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Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae: Chlamydophila.
                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OLIGOPEPTIDE BINDING PROFEIN.
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EMBL: AF002845; BAA98408.1; --
InterPro: IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Mhite O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Elsen J., Fraser C.M.;
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                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PEPTIDE ABC TRANSPORTER, PERIPLASMIC PEPTIDE-BINDING PROTEIN.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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EMBL; AE002215; AAF38388.1; -
TIGR; CP0569; -
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STAIN-MONN / NIGS.

MEDLINE-20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

Gwinn M., Nelson W., Debby R., Kolonay J., McClarty G., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 LSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGTYAF 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QRILQSKSLPIAS-GAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 QITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 ALSLAIDRETLLK--LAGKGSIATSFVHPSLSKMPLDVLSQ-KERISLAKNYLAEALK-- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 TVPQGELKKITLIYPIBSIVLRAVVQEIRQQLFDVLGFKISTLGLEYHSFLDKRSKGEFS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LATGGWFADFADPWAFLTIFAYPSGVPPYAI ---NHKDFLEILQN--IEQEQDHQKRSEL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSTGNWVADYQQAKAFLSILGNGTKYKDYQVIDWQNQEYTDIVSRLLVEDSTDLQILAE- 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PEPTIDE ABC TRANSPORTER, PERIPLASMIC PEPTIDE-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae Ax39.", Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE002313; AAF39300.1; -.
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                                       PRT;
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Pfam; PF00496; SBP_bac_5; 2.
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SEQUENCE 527 AA; 60452 MW;
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Best Local Similarity 35.33
Matches 185; Conservative
                                  PRELIMINARY;
                                                                                                                                                                                          Chlamydia muridarum
Bacteria; Chlamydia
                                                                                                                                                                                                                                         NCBI_TaxID=83560;
                                                        Q9PKL9;
                             O9PKL9
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STRAIN=D/UW-3/CX,
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 LSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 ALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHPLKLLALPVFFPVHKSQRT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 SLALIKNSHAVLTGALPVEDLGVRALNAKTLEIVLENPFPYFLEILAHPVFYPVHTSLRE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 YYKDKRNKRVFPIISNGPFAIQCYEPQRYLLINKNPLYHAKHDVLLNSVCLQIVPDIHTA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEE 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 SLATGGWFADFADPMAFLTIFAYPSGVPPYAINHKDFLEL-----LQNIEQEQDHQKRS 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 SLATGNWIADYHQASAFLSVLG-----NGTRYKDFQLINWQNQKYTNIVAQLLIQESS 476
                                                                                                                                                                                                                                                                                                                                                  'Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 AKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 L----QSKSLPIAS-GAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.0%; Score 685.5; DB 16; Length 34.4%; Pred. No. 5.5e-43; Live 89; Mismatches 227; Indels
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                                                                   Last sequence update)
Last annotation update)
                                                                                                                     OPPA_2 OR CT175.
Chlamydia trachomatis.
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                  OLIGOPEPTIDE BINDING PROTEIN PERMEASE.
                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001291; AAC67766.1; -...
InterPro: IPR000914; SBP_bac_5.
Pfam; PF00446; SBP_bac_5; 2.
complete proteome.
SEQUENCE 529 AA; 60331 MW;
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Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.";
Science 282:754-759(1998)
    PRELIMINARY;
                                                               01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                       01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=813;
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084178
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RESULT 097046

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15;
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STRAINA-ATCC 824 / DSM 792 / VKM B-1787;
MFDLINE=21359325; pubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng O., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y., Bennett G.N., Koonin E.V., Smith D.N.;
Genome sequence and comparative analysis of the solvent-producing J. Bacterium Clostridium acetobutylicum.,
J. Bacteriol. 187:14182-4838(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKL-KSAFWSNGDPLTAEDFIE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYIENAFEGLV-DINKNEKVVPGVASSWDISADNLTYTFHLRKNAKWSDGKPVKAKDFFF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWKQVATQEVSGIXAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLK 177
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123 AWKRALAPETASDYAYQLYYLKNGEAYNNGKASKDDVGVKAIDDYTLKVNLEAPTPYFLS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 LLALPVFFPVHKSORTLQSKSLP----IASGAFYPKNIKQKQWIKLSKNPHYYNQSQV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 ETKTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSW 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RKISVOICITILLSL-SVVLQGCKESSHSSTSRGE--LAINIRDEPRSLDPRQVRLLSEI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 KLNSITYYMLAQESSATAAFTSGQVD-----INDLIPAVQKSSLIQKGDAKAYPYYGTYF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 LTFNIN-----KFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNI-- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 FDINVGDKDSANGAEITKTLKNPKVREALNLAVDRESIVKNVTKGGEKPAISFVPSSIKL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 -----HSYPEHQKQEMAQRQAYAKKLFKEA-----LEBLQ11AKDLEHLNLIFP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 VSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 --GSNNQDVVQALQDMYKKNLNINFTLQSVERKVQLDNLTKQQYQICRASWLADYNDPMT 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 FLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQA-SLYLETFHIIEPIYH 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 PNGKTFKNKDYYP--AKGDVKK----AKQLLAEAGYPDGKGFPSWQIMYNE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
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19.6%; Score 536.5; DB 16; Length 550;
Best Local Similarity 26.8%; Pred. No. 8.1e-32;
Matches 153; Conservative 121; Mismatches 232; Indels 65;
                             01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLREL. 19, Last annotation update)
01-DEC-2001 (TREMSPORTER, PERIPLASMIC SUBSTRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     550 AA; 61190 MW; 3A7A48AD99C6C051 CRC64;
            550 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
Complete protecome.
          PRT;
     PRELIMINARY;
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01-OCT-2001 (
01-DEC-2001 (
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98 KLK-SAFWSNGDPLTAEDFIESWKQVATQEVSGIYA-FALNPIKNVRKIQEGHLSIDHFG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 VHSPNESTLVVTLESPTSHFLKLLALPVF--FPVHKSQRTLQSKSLP---1ASGAFYPKN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 RIPNEKYVVEKNDKYYNSNQVEVQEITFYTTNDSSTAXKMYENKELD---AIFGS-IPPD 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 TLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 LIKDLKLRSDYYSSAVNAIXFYAFNTYIKPLDNVKVRKALTLAIDRETLTYKV-LDNGTT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 INIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 PTRRIADNFSSY-----SYAKNLELENPEJAKTLLAEAGYPNGN-GFPILKLK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 ADHLLPTNIHSYPEHQKQEMAQRQAYAK--KLFKEALEELQITAKDLEHLNLIFPV---- 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 YNTSEAHKKICEFIQNQWKKILNIDVELENEEWTTYLNTRSNGNYEIARAGWIGDYADPL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 AFLTIFAYPSGVPPYAINH---KDFLEILONIEORODHOKRSELVSOA-SLYLETFHIIE 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 TFLSIFT--QGYTQFSSHNYSSPBYNELIKKSDLELDPIKRQDILRKABEIIIEKDFPIA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilske B., Habermann C., Fingerle V., Hillenbrand B., Jauris-Heipke S., Lehnert G., Pradel I., Roessler D., Schulte-Spechtel U.;
"An improved recombinant 1gG immunoblot for serodiagnosis of Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250013; CAB96045.1; -.
HSSP; P06202; 1B52.
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
SEQUENCE 528 AA; 60562 MW; AA6F2B802CBC46FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 28.6%; Pred. No. 7.9e-30;
Conservative 104; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.6%; Score 509.5; DB 2; 28.6%; Pred. No. 7.9e-30.
                                                                                                                                                                      528 AA.
520 YINVVEVKPYVKDLHKSPLGFVYFNNTYIKK 550
                                                                                                                                                                                                                          Created)
                                                                                                                                                                      PRT;
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                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                              Borrelia garinii.
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Matches 138;
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492 PIY 494
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Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                          Bacteria; Spiro
NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 RKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVF--FPVHKSQRTLQSKSL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 P---IASGAFYFKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIFDANTAAKLFNQGKL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 PENIVTSGPFKLKERIPNEXYVVEKNDKYYNSNQVEVQEITFYTTNDNSTAYKMYENGEL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 NWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KEEKKEGVS---FKISLGAEPSSLDPQLADDNVGSKMIDTMFKGLITGDPNTGGNKPGLA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 D----AIFSAIPPDLIKDLKLKSDYYSSAVNAIYFYAFNTHIKPLDNVKVRKALTLAIDR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 EALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAK - KLFKEALEELQITAKD 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 ETLITYKV-LDDGTTPTRRITPNFSSY-----SYAKNLELFNPEIAKTLLAEAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEHLNLIFPV-----SSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 YPNGN-GPPILKLKYNTSEAHKKICEFIQNQWKKILNIDVELENEEWITYLNTKSNGNYE 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LATGGWFADFADPWAFLTIFAYPSGVPPYAINH---KDFLEILQNIEQEQDHQKRSELVS 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 KESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSGNIEPALA 83
                                                                                                                                                                                                                                                     An improved recombinant IgG immunoblot for serodiagnosis of Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 28.0%; Pred. No. 1.4e-29;
Matches 139; Conservative 106; Mismatches 210; Indels
                                                                                                                                                                                                                                                                       borreliosis.";
Submitted (NOY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250012; CAB96044.1; -.
HSSP; P06202; 1B52.
                                                                                                                                                                                                                                                                                                                             InterPro; IRR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
SEQUENCE 528 AA; 60509 MW; E2D048F7290A7A16 CRC64;
                                                                                                                                                                                            STRAIN=PKO;
Wilske B., Habermann C., Fingerle V., Hillenbrand B.,
Jauris-Heipke S., Lehnert G., Pradel I., Roessler D.,
Schulte-Spechtel U.,
                                                                                                                                      Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=29518;
                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            18.5%; Score 506; DB 2; 28.0%; Pred. No. 1.4e-29;
                      528 AA.
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                                                  Created)
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                                          01-0CT-2000 (TrEMBLrel, 15, 01-0CT-2000 (TrEMBLrel, 15, 01-DEC-2001 (TrEMBLrel, 19,
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                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                          Borrelia afzelii.
                                                                                          SURFACE ANTIGEN.
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                 09K5J9
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031305
ID 031305
AC 031305
DT 01-JAN
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Q9K5J9
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98 KLKSAF-WSNGDPLTAEDFIESWKQVATQEVSGIYA-FALNPIKNVRKIQEGHLSIDHFG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 KNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 QETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 KTADHLLPTNIHSYPEHQKQEMAQRQAYAK--KLFKEALEELQITAKDLEHLNLIFPV-- 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 ----SSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFAD 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMAFLTIFAYPSGVPPYA---INHKDFLEILQNIEQEQDHQKRSELVSQA-SLYLETFHI 496
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                                                                                                                                                                                                                                                                                             Bono J.L., Tilly K., Stevenson B., Hogan D., Rosa P.;
"Oligopeptide permease in Borrelia burgdorferi: putative peptide-
binding components encoded by both chromosomal and plasmid loci.",
Microbiology 144:1033-1044(1998).
BNBL; AF000366; AAC46283.1; -..
HSSP; P06202; BB2.
InterPro; IPR000994; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
SEQUENCE 528 AA; 60560 MW; 9BC9A0B0382363DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.5%; Score 505.5; DB 2; Length 5 Best Local Similarity 28.0%; Pred. No. 1.6e-29; Matches 136; Conservative 109; Mismatches 197; Indels
01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                              Spirochaetales; Spirochaetaceae; Borrelia
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054584;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2004 (TrEMBLrel. 17, Last annotation update)
01IGOPEPTIDE PERMEASE PERIPLASMIC BINDING PROTEIN.
PLPB OR BB0329.
                                                                                                             Borrelia burgdorferi (Lyme disease spirochete)
                              01-JUN-2001 (TrEMBLrel. 17, Last an OLIGOPEPTIDE PERMEASE HOMOLOG AII.
                                                                                                                                                                                                                                                                          MEDLINE=98240240; PubMed=9579077;
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15;
                                                                                                                  STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Pougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
Van Vugt R., Painer N., Adams M.D., Gocayne J.D., Weidman J.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 KLKSAP-WSNGDPLTAEDFIESWKQVATQEVSGIYA-FALNPIKNVRKIQEGHLSIDHFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 VHSPNESTLVVTLESPTSHFLKLLA----LPVFFPVHKSQRTLQSKSLP---IASGAFYP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 KNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIP 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 QETLSNLQSKGHLHSFDVAGTSWLIFNINKFPLNNMKLREALASALDKEALVSTIFLGRA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 KTADHLLPTINIHSYPEHQKQEMAQRQAYAK--KLFKEALEELQITAKDLEHLNLIFPV-- 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 TIPTRRATPNESSY-----SYAKSLELENPEIAKTLLAEAGYPNGN-GFPILK 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 KERIPNEKYVFEKNNKYYDSNEVELEEITPYTTNDSSTAYKMYENEELD---AIFGS-IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 ----SSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 LKYNTNEANKKICEFIQNQMKKNLNIDVELENEEWTTYLNTKANGNYELARAGWIGDYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 528;
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18.5%; Score 505.5; DB 16; Length
Best Local Similarity 28.0%; Pred. No. 1.6e-29;
Matches 136; Conservative 109; Mismatches 197; Indels
                                                                                         Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                          528 AA; 60662 MW; C13627AA90B34BE6 CRC64;
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
Complete proteome.
SEQUENCE 528 AA, 60662 MW; (
                                                                                                                                                                                                                                                                                                    burgdorferi.";
Nature 390:580-586(1997),
EMBL; AF043071; AAC34991.1; -.
                                                                              J., Oliver D.;
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                                            SEQUENCE FROM N.A.
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Read T.D., Brunham R.C., Short, Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher R., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
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MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 VHKSQRILQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANT 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  :66
                                                                                                                                                                                                                                                                                                                                                                         "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-GOPEPTIDE BINDING PROFEIN
OPPA_3 OR CPN0197 OR CP0570.
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27.0%; Pred. No. 6.2e-28;
tive 92; Mismatches 190;
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Pfam; PF00496; SBP_bac_5; 4.
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SEQUENCE 435 AA; 50047 MW;
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Best Local Similarity 27.0%
Matches 141; Conservative
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216 AIHLLNRGKVDWVGQPWHQGIPWEL--HKQSQYHYYTYPVEGAFWLCLNTKSPHLNDLQN 273
                             307 REALASALDKEALVSTIFIGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALE 366
                                                           274 RHRLATCIDKRSIIEEALQGTQQPAETL-----SRGAPQPNQXKK----- 313
                                                                                         367 ELQITAKDLEHLNLIFPVSSSASSILLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGN 426
                                                                                                               314 --QKPLIPQEKLVLTYPSDILRCQRIABILKEQWK-AAGIDLILEGLEYHLFVNKRKVQD 370
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MEDLINE-21396508; PubMed-11481431;
MEDLINE-21396508; PubMed-11481431;
MEDLINE-21396508; PubMed-11481431;
Vorhoeller F.J., Hernardez-Lucas I., Becker J., Chain P.,
Vorhoeller F.J., Hernardez-Lucas I., Becker A., Cowle A., Gouzy J.,
Golding B., Pueller A.,
The Complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbioth Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. US.A. 98:9889-9894(2001).
EMBL; AL205269; CAC49261.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 AFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQECHLSIDHFGVHSPNE 161
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
NCBL_TAXID=382;
                                                                                                                                                                                                                                                                                                                                                            01-UNN-2001 (Tremblrel. 17, Created)
01-UNN-2001 (Tremblrel. 17, Last sequence update)
01-DEC-2001 (Tremblrel. 19, Last annotation update)
01-DEC-2001 (Tremsporter (PUTATIVE OLIGOPEPTIDE UPTAKE ABC
TRANSPORTER PERIPLASMIC SOLUTE-BINDING PROTEIN).
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Pfam: PF00496; SBP_bac_5; 1.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 532 AA; 59004 MW; FA0A382E4027D691 CRC64;
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                                                                         SK--GHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHL 334
                                                                                                            335 LPTNIHSYPEHQKQEMA----ORQAYAKKLFKEALEELQITAKDLEHLNLIFPVSSSAS 389
                                                                                                                                                                   -SLLVQLIREQWKESLGFAIPI----VGKEFALLQADLSSGNFSLATGGWFADFADFMAF 444
                                                                                                                              386 HERVATAVADMWKNTFGAKVSLVNLDVSSHYAYLQ---EGGKFNVARAGWVADYADAENF 442
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

RESULT A72107

peptide ABC transporter, periplasmic peptide-binding protein, probable CP0572 [import C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

Qy B Ωy 뭣 Qy ₽ Qy B A;Gene: oppA_1; CP0572 C;Superfamily: dipeptide transport protein A;Cross-references: GB;AE001606; GB:AE001363; NID:94376464; PIDN:AAD18348.1; PID:9437 A;Experimental source: strain CWL029 R;Read, T.D.; Bruhham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicker, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber, Nucleic Acids Res. 28, 1397-1406, 2000 A;Tittle: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR3; Reference number: A81500; MUID:20150255 A; Experimental source: strain AR39, HL cells A; Cross references: GB:AE002216; GB:AE002161; NID:97189484; PIDN:AAF38391.1; PID:9718 C; Genetics: A;Residues: 1-532 <REA> A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-532 <ARN> R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Tille: Comparative genomes of Clamydia pneumoniae and C. trachomatis. C;Accession: A72107; A81562 R;Kalman, S.; Mitchell, W.; A; Accession: A81562 A;Reference number: A7200; MUID:99206606 A;Accession: A72107 Matches Query Match Best Local Similarity 241 IPDANTAAKLENQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFP 181 LPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQXQWIKLSKNPHYYNQSQVETKTITIHF 181 LPVFEPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHF 240 121 QVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLA 180 121 QVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLIA 180 61 VKHIYEGIYQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWK 120 61 VKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTABEDFIESWK 120 1 MRKISVGICITILLSLSVYLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISL 60 MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISL 60 532; Conservative 100.0%; Score 2739; DB 2; 100.0%; Pred. No. 1.4e-187; 0; Mismatches 0, Length 532; Indels 0 Gaps 300 0;

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A;Residues: 1-532 <STO>
A;Cross-references: GB:BA000008; NID:g8978568; PIDN:BAA98405.1;
A;Experimental source: strain J138
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                                        FKEALEELQITAKDLEHLNLIFPYSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQA
                                                                                                                     LNNMKLREALASALDKEALYSTIFLGRAKTADHLLPTNIHSYPEHOKOEMAQROAYAKKL 360
                                                                                             LNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKL
                                                          FKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIDIVGKEFALLQA 420
                                                                                                                                                 IPDANTAAKLENQGKLNWQGPPWGERIPQETLSNLQSKGHLHSEDVAGTSWLTENINKEP
                                                                                                                                                                    IPDANTAAKLENQGKLNWQGPPWGERIPQETLSNLQSKGHLHSEDVAGTSWLTENINKEP
                                                                                                                                                                                                                      LPVFEPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHE
                                                                                                                                                                                                       LPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHF
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                                                                                                                                                                                                                                                                             OVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGYHSPNESTLVVTLESPTSHFLKLLA 180
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C:Genetics:
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A;Molecule type: DNA
A;Residues: 1-518 <ARN>
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A; Title: Genome sequence of
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R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitc)
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C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 21-Jan-2000
C;Accession: B71545
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                          476 DHOKRSELVSQASLYLETFHIIEPIYHDAFOFAMNKKLSNLGVSPTGVVDERYAKEN 532
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                                                                                                   416 ALLQADLSSGNFSLATGGWFADFADFMAFLTIFAYPSGVPDYAINHKDFLEILQNIEQEQ 475
                                                                                                                                                       343 LAKSLLEBALTELNMTIEDLEKYPLTFSATSTMNSQIAQMLRDQWRRSLGITFPICGKEY
                                                                                                                                                                                            356 YAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEF 415
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NPQKRSALISEASLYIERQNVIEPLYHDVFHYTTNNKLSFVRLHPSGLVDMRYAKNS
                                                                          ALLQNDLIGNTFFMSIGGWFADFSDPLAFLSIFS-SKGVKPYALQDPQFDQLILSIETEK
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E81699

peptide ABC transporter, periplasmic peptide-binding protein, probable TC0471 [imporC;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

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A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis A; Reference number: A72000; MUID: 99206606
                                                                                                                                                                       peptide ABC transporter, periplasmic peptide-binding protein, probable CP0571 [imported. C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: B72107; C81564
                                            A; Molecule
                                                              A; Accession: B72107
A; Status: preliminary
                                                                                                                                                                                                                                                                                     RESULT
B72107
                                                                                                                                          R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Nature Genet. 21, 385-389, 1999
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A;Title: Genome sequences of Chlamydla trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
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C;Superfamily: dipeptide transport protein
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C:Accession: E81699
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Best Local :
                                                                                                                                                                                                                                                                                                                                                      475 QDHQKRSELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFRYAKEN 532
                                                                                                                                                                                                                                                                                                                                                                                                                                         404 YALLQNDLTTNTFFMSINGWFADESDPLAFLSVFS-SKGIKPYALQDPLFDQLILSIETE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 ILAKTLIQEALTDLNMTIKDLEKCPLIFSATSSVNSQMAQMMRDQWRRILGITEPICGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 TITIHFIPDANTAAKLENQGKLNWQGPPWGERIPQETLSNLQSKGHLHSEDVAGTSWLTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 VRSWNDVLQNRIASIYSFAFLPI-----DLSKD-CGFFAKDN9TLVINLHTPTPHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FALLQADLSSGNESLATGGWEADPADPMAFLTIFAYPSGVDPYAINHKDELEILQNIEQE 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIHIHVIPDQQTASALFKQGKLDWQGLPWGHSIPQEALATANKRRTPQSFDISGTSWLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTSKVPFSHPKLRQALSLVLNKEALASPTFV----KPAKHLLPTHLHTYPEQPTYKQQEAV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKLLTLPVFYPVHPEHQIRNEAKALPISTGAFCLKEKKDRRWLKLEKNPYYYNKEQVAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKLLALPVFFPVH-KSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDINLIHHLYEGLVQETP-SGEVFPALAESFFLSEDKKTYTFHLKKALWSNGDLITAHDF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEISLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRKVSVGTC--LLIALATAITGCSKSSSNKSNHSSSNQ-SVSVSMKDDPRTFDPREVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.1%; Score 1345; DB 2; 49.4%; Pred. No. 4e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 520
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                                                                                                                                                          Olinger, L.;
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                                                                                                                                                        Grimwood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                oligopeptide binding protein [imported] - Chlamydophila pneumoniae (strain J138) C.Specles: Chlamydophila pneumoniae, Chlamydia pneumoniae C.Pate: 02-Mar-2001 sequence_revision 02-Mar-2001 *text_change 02-Mar-2001 C.Accession: D85515 |
C.Accession: D85515 |
R.Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A; Reference number: A86491; MUID:20330349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-527 <ST(
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C;Superfamily: dipeptide transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE002215; GB:AE002161; A;Experimental source: strain AR39, HL cells
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A; Residues: 1-527 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255 A;Accession: C81564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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Best Local Similarity
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486 LEHCHILEPLCHPNLRIALNKNIKNFNLFVRRTSDFRFIEK
                                      491 LETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFRYAKE 531
                                                                                426 VNQWTAAFIDPMSYLMIFANPGGISPYHLQDSHFQTLLIKITQEHKKHLRNQLIIBALDY
                                                                                                                                                                      366 TREDLEKETLTFSTFSFSYGRICQMLREQWKKVLKFTIPIVGQEFFTIQKNFLEGNYSLT 425
                                                                                                                         431 TGGWFADFADPMAFLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLY
                                                                                                                                                                                                  371 TAKDLEHLNLIFPVSSSASSILVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLA 430
                                                                                                                                                                                                                                                                                 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TEWLITSGC---SPSQSSKGIFVVNMKEMPRSLDPGKTRLIADQTLMRHLYEGLVEEHSQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNL 74
                                                                                                                                                                                                                                                              AIDKDMLTKVVYQGLAEPTDHILHPRLYPGTYPERKRQN--ERILEAQQLFEEALDELQM 365
                                                                                                                                                                                                                                                                                                                                                        QGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALAS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                              STSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHNKSRVKLHKIIVQFISNANTAAILFK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLPIKNARAIFDDTESPENLGVRALDKRHLEIQLETPCAHFLHFLTLPIFFPVHETLRNY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGEIKPALAESYTISEDGTRYTFKIKNILWSNGDPLTAQDFVSSWKEILKEDASSVYLYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QS--KSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAAKLFN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.4%; Score 1160.5; Dilarity 43.2%; Pred. No. 6e-75; Conservative 111; Mismatches 1
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                                                                                                                 C;Genetics:
A;Gene: oppA_4
C;Superfamily: dipeptide transport protein
                                                                                                                                                                                                                                                                                                       oligopeptide binding protein - Chlamydophila pneumoniae (strain CWL029) (Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c.) Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C:Accession: D72107 R:Kalman, S: Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-526 <ARN>
A;Cross-references: GB:AE001606; GB:AE001363; NID:g4376464; PIDN:AAD18351.1; PID:g43764
                                                                                                                                                                              A; Experimental source: strain CWL029
                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                             A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis A; Reference number: A72000; MUID:99206606
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A;Experimental source: strain J138
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     13 LLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQEN 72
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 LEHCHILEPLCHPNLRIALNKNIKNFNLFVRRTSDFRFIEK 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 TGGWFADFADPAAFLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLY 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 TAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 HKKLDWOGDPWGEPIPPEISASLHQDDQLFSLPGASTTWLLFNIQKKPWNNAKLRKALSL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 AIDKDMLTKVVYQGLAEPTDHILHPRLYPGTYPERKRON--ERILEAQQLFEEALDELQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 ALDKEALVSTIFLGRAKTADHLLPTNIH--SYPEHQKQEMAQRQAYAKKLFKEALEELQI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 OGKLNWOODPWGERIPOETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALAS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 QS--KSLPTASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAAKLEN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 LNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TLWLITSGC---SPSQSSKGIFVVNMKEMPRSLDPGKTRLIADQTLMRHLYEGLVEEHSQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 SLSVYLOGCKESSHSSTSRGELAINIRDEPRSLDPROVRLLSEISLVKHIYEGLYQENNL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                       177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TREDLEKETLTESTESBSYGRICOMLREQWKKVLKETIPIVGQEFFTIQKNFLEGNYSLT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSFEEMPITCGAFRPVSLEKGLRLHLEKNPMYHNKSRVKLHKIIVQFISNANTAAILEK 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 111; Mismatches 176; Indels
                                                              27.6%;
33.9%;
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43.2%; Pred. No. 6e-75;
                                                106;
                                         Score 755.5; DB 2;
Pred. No. 4.8e-46;
% Mismatches 216;
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                                         Indels
                                                                         Length 526;
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                                    Gaps
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cligopeptide binding protein [imported] - Chlamydophila pneumoniae (strain J138) C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c.Species: Chlamydophila pneumoniae C.Pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 K.Shirai, F. Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: oppA_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:BA000008; NID:g8978571; PIDN:BAA98408.1; GSPDB:GN00142
A:Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-526 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138
A;Reference number: A86491; MUID:20330349
A;Accession: F86515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
                                                         132 TLLGVIKNSSAIHNAQKSLETLGTQAKDDLTLVITLEQPFPYFLTLIARPVFSPVHHTLR 191
193 TLQSKSLP----IASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAA 248
                                                                                              133 FALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQR 192
                                                                                                                                                                   73 NLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYA 132
                                                                                                                                                                                                                                                                             15 LLFLLITLSSCSKQKQEPLGK-HLVIAMSHDLADLDPRNAYLSRDASLAKALYEGLTRET 73
                                                                                                                                                                                                                                                                                                                                   13 LLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQEN 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 LATGGWFADFADPMAFLTIFAYPSGVPPYAINHKDFLEILQNI---EQEQDHQKRSELVS 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 QITAKDLEHLNLIFÞVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 AIAHAIDRKSILRLVPSG--QEAVTLVPPNLSQLNLQKEISTEERQTKARAYFQEAKETL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 ALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEEL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 KLFKSKSIDWIGSPWSAPISNED-QKVLSQEKILTYSVSSTTLLIYNLQKPLIQNKALRK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 KLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLRE 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 FALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSOR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 TLQSKSLP----IASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 TLLGVIKNSSAIHNAQKSLETLGIQAKDDLTLVITLEQPFPYFLTLIARPVFSPVHHTLR 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         27.6%; Score 755.5; DB 2; 33.9%; Pred. No. 4.8e-46;
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C;Superfamily: dipeptide transport protein
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;CTOSS-references: GB:AE002215; GB:AE002161; NID:g7189472; PIDN:AAF38388.1; PID:g718948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-528 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide ABC transporter, periplasmic peptide-binding protein CP0569 [imported] - Chlamyd C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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Best Local
     313 AIAHAIDRKSILRLVPSG--QEAVTLVPPNLSQLNLQKEISTEERQTKARAYFQEAKETL
                                   309 ALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHOKQEMAQRQAYAKKLFKEALEEL 368
                                                                                     254
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                                                                                                                                                                                                         134 TLLGVIKNSSAIHNAQKSLETLGIQAKDDLTLVITLEQPFPYFLTLIARPVFSPVHHTLR
                                                                                                                                                                                                                                     133 FALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFFVHKSQR 192
                                                                                                                                                                                                                                                                          76 D--QGIALALAESYTLSKDHKYYTFKLRPSVWSDGTPLTAYDFEKSIKQLYFEEFSPSIH 133
                                                                                                                                                                                                                                                                                               73 NLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFLESWKQVATQEVSGIYA 132
                                                                                                                                                                                                                                                                                                                                           17 LLFLLLTLSSCSKQKQEPLGK-HLVIAMSHDLADLDPRNAYLSRDASLAKALYEGLTRET
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                    KLFKSKSIDWIGSPWSAPISNED-QKVLSQEKILTYSVSSTTLLIYNLQKPLIQNKALRK 312
                                                                                                    KLFNQKKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNWKLRE
                                                                                                                                                                    TLQSKSLP----IASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAA 248
                                                                                                                                       ESYKKGTPPSTYISNGPFVLKKHEHQNYLILEKNPHYYDHESVKLDRVTLKIIPDASTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IATGGWIAEYVSPVAFLSILGNPRDLTQW--RNSDYEKTLEKLYLPHAYKENLKRAEMI- 483
                                                                                                                                                                                                                                                                                                                                                                                                                            177;
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33.9%;
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Pred. No. 4.8e-46;
D6; Mismatches 216;
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A:Gene: TC0446
C:Superfamily: dipeptide transport protein
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R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002313; GB:AE002160; NID:g7190484; PIDN:AAF39300.1; PID:g719A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide ABC transporter, periplasmic peptide-binding protein TC0446 [imported] - Chla (Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-527 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
A;Accession: H81701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
484 VSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFR 527
                                                                                                                                                       364 TVPQEELKKITLIYPIESIVLRAVVQEIRQQLFDVLGFKISTLGLEYHSFLDKRSKGEFS
                                                                                                                                                                                                                                                                                                                                                                                   250 QLFQKKYYDLVGLFWSSSFPLEEQKNL-SQDFLYDYPVLNCTVLFCNVNHKPLDNPSLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                    249 KLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLRE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 YYRNRSKRSLPIISNGPFIIRCYEPQNFLLLDKNPFYHDQKNVSLDAVRLQIVPDIHTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 ALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFEPVHKS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 --GSLHLALAERYSISQDRCVYTFFLKKTFWHNGDLVTAYDFEESIKQFYLHEVDNVALR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 LSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 LSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPROVRLLSEISLVKHIYEGLVQENN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 --SEKELAELSILYPIDSSNSSIIAQEIQRQLKDTLGLKIKIQGMEYHCFLKKRRQGDFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 QITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                             QITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFS 428
                                                                                                                                                                                                                                                                                                                       ALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLEKEALEEL
                                                LSTGNWVADYQQAKAFLSILGNGTKYKDYQVIDWQNQEYTDIVSRLLVEDSTDLQILAE-
                                                                                                 LATGGWFADFADPMAFLTIFAYPSGVPPYAI---NHKDFLEILQN--IEQEQDHQKRSEL 483
                                                                                                                                                                                                                                                                    ALSLAIDRETLLK--LAGKGSIATSFVHPSLSKMPLDVLSQ-KERISLAKNYLAEALK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ORTLOSKSLPIAS-GAFYPKNIKOKOWIKLSKNPHYYNQSQVETKTITIHFIPDANTAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLALIKNSHAVLKGDIPVENLGVRALDEHTLEITLEHPSSHFLETLTHPVFYPVHASLRE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSLTFGLTSCHQKEEN--LRNILRVAICHDPMSLDPRQVFLIKDVCIAKALYEGLVREND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185;
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Pred. No. 1.6e-45
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N;Alternate names: opph homolog; sporulation initiation protein spo0KA C;Species: Bacillus subtilis C;Cate: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 20-Jun-2000 C;Accession: A38447; S15230; G69668
                                                    oligopeptide ABC transport system substrate-binding protein oppA precursor - N:Alternate names: oppA homolog; sporulation initiation protein spo0KA
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C:Superfamily: dipeptide transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE001291; GB:AE001273; NID:g3328573; PIDN:AAC67766.1; PID:g33285:A;Experimental source: serotype D, strain UW-3/Cx C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-529 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Title: Genome sequence of an obligate intracellular pathogen of A:Reference number: A71570; MUID:99000809
A:Accession: F71547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Stephens, R.S.; Kalman, S
Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable oligopeptide binding protein - Chlamydia trachomatis (serotype D, strain C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 21-Jan-2000 C;Accession: F71547
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Best Local Sim
Matches 181;
                                                                                                                                                                                              477
                                                                                                                                                                                                           482 ELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFR 527
                                                                                                                                                                                                                                            424 SLATGNWIADYHQASAFLSVLG-----NGTRYKDFQLINWQNQKYTNIVAQLLIQESS
                                                                                                                                                                                                                                                                                                                                                       368 LQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENN 73
                                                                                                                                                                          DLQLMAEQLLLKESPLIPLYHLDYVYAKQPRVSDLQTSSRGEIDLK 522
                                                                                                                                                                                                                                                                               SLATGGWFADFADPMAFLTIFAYPSGYPPYAINHKDFLEI-----LQNIEQEQDHQKRS 481
                                                                                                                                                                                                                                                                                                                    L--SQEDLEKITLIYPIESVCLRAVVQEIRQQLFDVLGFKISTLGLEYHCFLDKRSRGEF
                                                                                                                                                                                                                                                                                                                                                                                          TALSLAINRETLLK--LAGKGCSATSFVHPQLSQIPATTLSQ-DERIALAKGYLTEALKT
                                                                                                                                                                                                                                                                                                                                                                                                                               EALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKLENQGKLNWQGPPWGERIPQETLSNLQSKGHLHSEDVAGTSWLTFNINKFPLNNMKLR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYKDKRNKRVFPIISNGPFAIQCYEPQRYLLINKNPLYHAKHDVLLNSVCLQIVPDIHTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-----QSKSLPIAS-GAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA--FQLALAERYHQSDDGCVYTFFLKNTFWSNGDVVTAYDFEESIKQIVFREIDNPSLR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 68
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Pred. No. 4.8e-41;
99; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 529;
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                                                                         Bacillus
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Дb
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                                 234
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C;Superfamily: dipeptide transport protein (Keywords: blocked amino end; lipoprotein; membrane protein; oligopeptide transport; F;1-20/Domain: signal sequence #status predicted <SIG> F;21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted F;21/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain 168
A;Note: (initiation of sporulation, competence development)
C;Comment: This operon of five genes is homologous to the oligopeptide permease opero enetic competence by sensing extracellular peptide factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Ehrlich, S.D., Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Cardino, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete A.; Authors: Schleich, S.; Schloeter, R.; Scoffone, F.; Sakiguchi, J.; Sakowska, A.; See T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
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A;Molecule type: DNA
A;Residues: 1-25,'T',27-194,'E',196-339,'M',341-545 <PER>
A;Residues: 1-25,'T',27-194,'E',196-339,'M',341-545 <PER>
A;Cross-references: EMBL:X56347; NID:940004; PIDN:CAA39787.1; PID:940005
A;Cross-references: EMBL:X56347; NID:940004; Alloni, G.; Azevedo, V.; Carter, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.;
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, B.; Caquano, V.; Carter, N.M.;
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Caquano, V.; Carter, N.M.;
C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
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A; Residues: 1-545 <KUN>
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A;Accession: S15230
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J. Bacteriol. 173, 1388-1398, 1991
A;Title: The spook locus of Bacillus subtilis is homologous to the oligopeptide perm.
A;Reference number: A38447; MUID:91139580
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Mol. Microbiol. 5, 173-185, 1991
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A; Residues: 1-545 < RUD>
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Best Local
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KKIDMYMINNNTELKKFQAGELDWAGMPLGQ-LPTESLPTLKKDGSLHVEPIAGVYWYK 304
                                                              KTITIHFIPDANTAAKLFNQGKLNWQGPFWGERIPQETLSNLQSKGHLHSFDVAGTSWLT
                                                                                                                                                                                                                                                                                 WALDPNNESQYAYQLYYIKGAEAANTGKGSLDDVAVKAVNDKTLKVELNNPTPYFTELTA
                                                                                                                                                                                                                                                                                                                                                QVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLA 180
                                                                                                                                                                                                       LPVFFPVHKSQRTLQSKSLPIASGAFYPKN--IKQKQW-----IKLSKNPHYYNQSQVET
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Pred. No. 3.6e-36;
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01490peptide ABC transporter, periplasmic substrate-binding component CAC3634
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C; Accession: B97346
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C;Superfamily: dipeptide transport protein
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A:Cross-references: GB:AE001437; PIDN:AAK81557.1; PID:g15026735; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
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J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A98900; MUID:21359325; PMID:21359325
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384 VSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPNA 443
                                      358 PNGKTFKNKDYYP--AKGDVKK----AKQLLAEAGYPDGKGFPSMQIMYNE-----
                                                                                                                  298 FDINVGDKDSANGAEITKTLKNPKVREALNLAVDRESIVKNVTKGGEKPATSFVPSSIKL
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                                                                                                                                                       LTFNIN-----KFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNI--
                                                                                                                                                                                                                                   ETKTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSW
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26.8%;
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Pred. No. 2.2e-30;
21; Mismatches 232;
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A:Experimental source: strain B31
C;Superfamily: dipeptide transport protein
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A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: H70140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 20-Aug-1999
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IEPIY 501
                                    PLTFLSIFT
                                                                                                                        ----SSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFAD 440
                                                                                                                                                                                                                                                      PDLIKNLKLRSDYYSSAVNAIYFYAFNTHIKPLDNVKIRKALTLAIDRETLTYKY-LDNG
                                                                                                                                                                                                                                                                                  QETLSNLQSKGHLHSEDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                    VHSPNESTLYVTLESPTSHFLKLLA----LPVFFPVHKSQRTLQSKSLP----TASGAFYP 208
                                                                                                                                                                                        TTPTRRATPNFSSY ---
                                                                                                                                                                                                              KTADHLLPTNIHSYPEHQKQEMAQRQAYAK--KLFKEALEELQITAKDLEHLNLIFPY--
                                                                                                                                                                                                                                                                                                                                  KERIPNEKYVFEKNNKYYDSNEVELEEITFYTTNDSSTAYKMYENEELD---AIFGS-IP
                                                                                                                                                                                                                                                                                                                                                                    KNIKOKOWIKLSKNPHYYNOSQVETKTITIHFIPDANTAAKLFNOGKLNWOGPPWGERIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTNVVEVKPYVKDLHKSPLGFVYFNNTYIKK 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQA-SLYLETFHIIEPIYH 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMDLFVTDSGNNNSGYSNPEYDALIKDAKTTNDADKRIDDMHKAEDAAMRDLPVI-PIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GSNNQDVVQALQDMYKKNLNINFTLQSVERKVQLDNLTKQQYQICRASWIADYNDPMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                        -QGYTQFSSHNYSNPEYNELIKKSDLELDPIKRQDILRQAEEIIIEKDFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%;
                                                                                                                                                                            -----SYAKSLELFNPEIAKTLLAEAGYPNGN-GFPILK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 505.5; DB 2;
Pred. No. 3.3e-28;
)9; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID: g2688225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAC66707.1; PID:g268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
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                                                                                                    431
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A:Note: the authors translated the codon GTG for residue 10 as B,
Leu, GTT for residue 182 as Glu, and ACA for residue 183 as Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: dipeptide transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Mathiopoulos, C.; Mueller, J.P.; Slack, F.J.; Murphy, C.G.; Patankar, S.; Bukusoglu, c.Mol. Microbiol. 5, 1903-1913, 1991
Mol. Microbiol. 5, 1903-1913, 1991
A;Title: A Bacillus subtills dipeptide transport system expressed early during sporulati
A;Reference number: S16646; MUID:92114768
A;Accession: S1665]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parco, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Tosato, V.; Uchlyama, A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Yata, K.; Yoshida, K.; Reference number: A69580; MUID:98044033

A; Cetatonomic 169618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: dppE; dciAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 7-271, 'K', 273-344, 'P', 346-549 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross references: GB:Z99110; GB:AL009126; NID:92633472; PIDN:CAB13153.1; PID:92633650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-549 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dipeptide ABC transporter (dipeptide-binding protein) - Bacillus subtilis C.Species: Bacillus subtilis C.Species: Bacillus subtilis C.Spacies: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000 C.Accession: G69618; S16651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-556, 197
309 FNVNMEDFQNENIRKAFAMAVDQEEIVKYVTKNNEKTA-HAFVSPGFTQPDGKDFREAGG
                                                           294 FNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQENA--
                                                                                                                      255 DKYKWAMYSDRNIDYQMFQSGELD-----TAYYPAELSDQLLDQDNYNIYDQAGLYFYR 308
                                                                                                                                                                                    234 KTITIHEIPDANTAAKLENQGKLNWQGPPWGERIPQETLSNLQSKGHLHSEDVAGTSWLT 293
                                                                                                                                                                                                                                                   195 VSNPAYFPVNEKVDKDNPKWFAESDTFVGNGPFKLTEWKHDDSITMEKSDTYWDKDTVKL 254
                                                                                                                                                                                                                                                                                                              179 LALPVFFPVHK-----SQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVET 233
                                                                                                                                                                                                                                                                                                                                                                            135 WKRMLDPKKGASSAFLGYFIEGGEAYNSGKGKKDDVKVTAKDDRTLEVTLEAPQKYFLSV 194
                                                                                                                                                                                                                                                                                                                                                                                                                       119 WKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 LALGLSFALMGCTANEQAGKEGSHDKAKTSGEKVLYVNNENEPTSFDPPIG--FNNVSWQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 ILLSLSVVLQGC------KESSH-SSTSRGE--LAINIRDEPRSLDPRQVRLLSEISL- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLNNIMEGLTRLGK-DHEPEPAMAEKWSYSKDNKTYTFTIRENAKWINGDPVTAGDFEYA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLK-SAFWSNGDPLTAEDFIES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143; Conservative 116; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.9%; Score 489.5; DB 2 26.0%; Pred. No. 4.9e-27;
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540 YIDLKWADKN 549
                                  523 VVDFRYAKEN 532
                                                             480 EYDQLIKQAKNEADEKTRFSLMHQAEELLINEAPIIPYYFYNQVHLQNEQVKGIVRHDVG 539
                                                                                                  463 DFLEILQNIEGEODHQKRSELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTG 522
                                                                                                                                         420 SLGVDVKLANMEWNVFLEDQKALKFQFSQSSFLPDYADPISFLEAFQTGNSMNRTGWANK 479
                                                                                                                                                                              403 SLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFLTIFAYPSGVPPYAINHK 462
                                                                                                                                                                                                                       368 DLIKPNESKAKQLIEKGMKE------ENYNKLPAITLTYSTKPEHKKIAEAIQQKLKN 419
                                                                                                                                                                                                                                                                              352
                                                                                                                                                                                                                                                         ----QRQAYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASS-----LLVQLIREQWKE 402
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Search completed: July 26, 2002, 04:39:59 Job time: 3802 sec

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Result
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Maximum
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Maximum Match 10
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Perfect score:
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                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
                  864
753.5
680.5
617.5
521.5
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DB seq length: 2000000000
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2645
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                 100.0

96.6

41.1

31.5

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22.5

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18.5
                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                          9: SIDSS/gcgdata/geneseq/geneseqp-emb1/AA198.DAT:*
10: SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
11: /SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
14: /SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
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15: /SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDSS/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRKISVGICITILLSLSVVL.....LSNLGVSPTGVVDFRYAKEN 532
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2739
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Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDS5/gcgdata/geneseq/geneseqp-embl/AA1983_DAT**
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Chlamydia pneumoni
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Chlamydia trachoma
B. burgdorferi ant
B. burgdorferi ant
Chlamydia pneumoni
                                                                                                                                                                                                                        Description
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| 209 | . = | 214.5 | ٠., | 263.5 | ١., | ್ಷ | 0 | ٠ - | | | 9 | 296.5 | | 303.5 | 308.5 | 321.5 | 329.5 | 349 | 351 | U | 371.5 | 3 | 390 | 9 | 393.5 | 394 | 403.5 | 414.5 | 417.5 | 421 | 425.5 | 15 | |
|--------------------|----------------|-------|------|-------|-----------|--------------------|-----------|----------------------------|----------|--------------------|----------|---------------|----------|----------|----------|----------|----------|--------------------|----------|--------------------------|----------|----------|-------------|----------|----------|------------|---------------|----------------|----------------|----------------|-------------------|----------|--------------------|
| 7.6 | | | | | | | | | | | | | | | | | | | | | | | | 14.3 | | 14.4 | 14.7 | ٠ | | 5 | 5 | | 16.6 |
| 615 | 705 | 503 | 556 | 314 | 278 | 549 | 549 | 643 | 535 5 | 537 | 343 | 321 | 524 | 342 | 381 | 372 | 373 | 526 | 406 | 546 | 310 | 522 | 532 | 514 | 521 | 550 | 542 | 541 | 553 | 506 | 523 | 528 | 547 |
| 22 | 22 | 22 | 22 | 18 | 22 | 22 | 19 | 97 | 22 | 22 | 20 | 20 | 22 | 20 | 22 | 20 | 20 | 20 | 20 | 20 | 20 | 15 | 20 | 20 | 20 | 22 | 20 | 20 | 20 | 20 | 20 | 20 | 20 |
| 582 | 9663 | 229 | 07 | 974 | 55 | AAU35720 | AAW98830 | AAR70152 | AAU38208 | AAU36431 | AAY00088 | AAY00089 | AAU34786 | AAY00061 | AAU03659 | AAY00060 | AAY00067 | AAY00051 | AAY00066 | AAY00050 | AAY37060 | AAR48035 | AAY00053 | AAY19989 | AAY00041 | AAU34906 | AAY00040 | AAY19988 | AAY00052 | AAY19871 | AAY19870 | AAY00031 | AAY00030 |
| Novel human diagno | oonde devitetu | | 2000 | | enidermid | Helicobacter pulor | nylori cu | reptococous zmonerra cy | יייטאיי | Pseudomonas acrusi | | terrocordinat | 1207 | ታ ር | B Stran | | | Enterococcus faeca | | eriococore eriococore | 7 (| 2 | nterococcus | 3. 5 | | terpoordis | ot topocousto | huradorferi an | nterococous fa | burgdorferi an | יו הייני מור ל | fapo | Enterococcus faeca |

ALIGNMENTS

RESULT AAE12212

Murdin AD, 04-APR-2000; 2000US-194464P 04-APR-2001; 2001WO-CA00455 (AVET) AVENTIS PASTEUR LTD. 11-OCT-2001. WO200174863-A2. Chlamydia pneumoniae. ATP-binding cassette; antibiotic; vaccine; infection; therapy; poxvirus. Chlamydia pneumoniae ATP-binding cassette protein. Region Region Region Key AAE12212 standard; Protein; 532 AA. AAE12212; 15-JAN-2002 Oomen RP, (first entry) /label= B-cell_epitope 469..482 338..359 /label= T-cell_epitope Location/Qualifiers 53..61 /label= B-cell_epitope Wang J, Dunn ₽;

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel Chlamydia pneumoniae ATP-binding cassette protein and its corresponding gene. Sequences of the invention care useful for detecting Chlamydia infection by assaying a body fluid conformation of a mammal with the components. They are also used as vaccines. ATP conformation components. They are also used as vaccines. ATP conformation conformation treating Chlamydia infection e.g. infection caused by C. trachomatis, C. psittaci, C. pneumoniae or C. pecorum in mammals, cuch as humans. The nucleic acid molecules are useful for producing CC ATP-binding cassettes, in the construction of vaccine vectors such cas powriruses, which are further useful for producing and/or treating CC chlamydia infection and in the construction of attenuated Chlamydia in that can over-express the nucleic acid molecules or express that can over-express the nucleic acid molecules or express it in a non-toxic, mutated form. The present sequence is ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Chlamydia ATP-binding cassette and corresponding DNA molecule for preventing, diagnosing and treating Chlamydia infections in mammals, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                   selvsqaslyletfhiiepiyhdafqfamnkklsnlgvsptgvvdfryaken 532
                                                                                                                                        DLSSGNESLATGGWEADFADPMAFLTIFAYPSGYPPYAINHKDFLEILQNIEQEODHQKR
                                                                       SELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDERYAKEN 532
                                                                                                                    \tt dlssgnfslatggwfadfadpmafltifaypsgvppyainhkdfleilqnieqeqdhqkr' \\
                                                                                                                                                                                                          FKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIRBQWKESLGFAIPIVGKEFALLQA
                                                                                                                                                                                        fkealeelqitakdlehlnlifpvsssassllvqlireqwkeslgfaipivgkefallqa
                                                                                                                                                                                                                                                         In {\tt nmklrealasald Kealvstifl graktad hilptnih sypehqk qemaqrqayakkl}
                                                                                                                                                                                                                                                                              LNNMKLREALASALDKEALVSTIFLGRAKTADHLLFTNIHSYPEHQKQEMAQRQAYAKKL
                                                                                                                                                                                                                                                                                                                           ip dantaakl fing gklnwqqppwgerip qetlsnlqskghlhsfdvagtswltfninkfp
                                                                                                                                                                                                                                                                                                                                                IPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFP
                                                                                                                                                                                                                                                                                                                                                                                                                   LPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKOKQWIKLSKNPHYVNOSQVETKTITIHE
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                                                                                                                                                                                                                                                                                                                                                                                                 {\tt lpvffpvhksqrtlqskslpiasgafypknikqkqwiklsknphyynqsqvetktitihf}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qvatqevsgiyafalnpiknvrkiqeghlsidhfgvhspnestlvvtlesptshflklla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt mrkisvgicitills lsvvlqgckesshsstsrgelainirdeprsldprqvrllseisl}
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                                   301
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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21-NOV-1997;
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vaccine; neutralising epitope.
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                                                                                                                                                                                                                                                                                                    1 MRKISYGICITILLSLSYYLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISL
ip dant a akl fnq gkln wqqpp wgerip qetlsnlqskghlhsfd vagtswltfninkfp
                                                                      IPDANTAAKLENGGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTENINKEP
                                                                                                           {\tt lpvffpvhksqrtlqskslpiasgafypknikqkqwiklsknphyynqsqvetktitihf}
                                                                                                                                      LPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHF 240
                                                                                                                                                                 qvatqevsgiyafalnpiknvrkiqeghlsidhfgvhspnestlvvtlesptshflklla 180
                                                                                                                                                                                                                       vkhiyeglvqennlsgniepalaedyslssdgltytfklksafwsngdpltaedfieswk
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                                                                                                                                                                               QVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLA
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Pred. No. 9e-232;
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RESULT AAY34797, ID AAY3
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XX AAY3
AC AAY3
XX Chla
XX Resp
KW Resp
KW Sinu
KW Vacc
OS Chla
XX VO99
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21-NOV-1997;
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Pred. No. 1.5e-93;
4; Mismatches 168;
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                                                                                                                                                                                     04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                       Genome sequence of Chlamydia trachomatis
                                                                                                                 WPI; 1999-371125/31.
                                                                                                                                           Griffais
                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                    27-NOV-1998;
                                                                                                                                                                                                                                                                                  W09928475-A2
                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                       Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis lipoprotein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-1999
                                                                                                                                                                                                                                                             10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY37005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY37005 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 nlfvrrtsdfrfiek 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61\ nilws ngdpl taqdfvs swkeilke das svyly aflpiknara if ddte spenl gyrald
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNL 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSKNPHYYNQSQVETKTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFLTIFAYPSGVPP
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                                                                                                                                                                                                  98US-0107077
97FR-0015041
                                                                                                                                                                                     97FR-0016034
                                                                                                                                                                                                                                    98WO-IB01939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as Yaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye

Disclosure;

Page 836; 1755pp; English.

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RESULT
AAY34799
ID AAY3
XX AAY3
AC AAY3
XX Chla
XX Chla
XX Resp
KW Sinu
XX Vacc
OS Chla
XX Vacc
OS Chla
XX Vacc
XX Vogc
XX Vogc
XX III
PF 20-1
XX PF 21-1
XX PF 21-1
XX WPI;
XX PF Grif
XX VPS Page
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                               04-NOV-1998;
21-NOV-1997;
Page 772-773; Disclosure; 1912pp; English.
                             Genome sequence of Chlamydia pneumoniae
                                                              WPI; 1999-357842/30
                                                                                          Griffais R;
                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                    03-JUN-1999
                                                                                                                                                                                                                                                                       Chlamydia pneumoniae
                                                                                                                                                                                        20-NOV-1998;
                                                                                                                                                                                                                                              W09927105-A2
                                                                                                                                                                                                                                                                                              vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                           sinusitis; purulent otitis media;
                                                                                                                                                                                                                                                                                                                         Respiratory disease; pneumonia; bronchitis;
                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae lipoprotein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY34799 standard; Protein; 534 AA
                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY34799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 ntakkpfshsklrgalslvlnkealaslafvxxckts 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 NINKFPLNNMKLREALASALDKEALVSTIFLGRAKTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 eicihiipdqqtasalfnqgkldwqglpwghsipqetlatankrrapqsfdisgtswltf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  may be of use in treating these diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 ESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLLALPVFFPVHKSQRTL--QSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITIHFIPDANTAAKLENOGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                klltlpvfypvh-sqhqiwkeekslpistgafflkekkdrrwlklekspyyynkdqvavq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dinlihhlyeglvqetp-sgevfpalaesfflsedkktytfnlkkafwsngdlitahdfv 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EISLVKHIYEGIVQENNISGNIEPALAEDYSLSSDGITYTFKLKSAFWSNGDPLTAEDFI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRKISVGICITILLSLSVVLQGCKESSHSSTSRG----ELAINIRDEPRSLDPRQVRLLS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rswndvlqnrvasiysfaflpi-dvnk----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mrkisvgiclllalats----gcsksssnathrspathtvavsvkddprtfdprevrlis 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174;
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                            98US-0107078.
97FR-0014673.
                                                                                                                                                                                     98WO-IB01890.
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51.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 864; DB 20;
Pred. No. 5.8e-70;
56; Mismatches 85
                                                                                                                                                                                                                                                                                                              erythema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---dsgffakddhtlvinlltptphfl
                                                                                                                                                                                                                                                                                                       nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                      heart disease; sarcoidosis;
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Best Local :
                  Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepa nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                          Chlamydia trachomatis lipoprotein sequence
                                                                                                                                                     07-OCT-1999
                                                                                                                                                                                           AAY37027;
                                                                                                                                                                                                                         AAY37027 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                                                                                                        492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 QITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 aiahaidrksilrlvpsg--qeavtlvppnlsqlnlqkeisteerqtkarayfqeaketl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 tllgviknssaihmaqksletlgiqakddltlvitleqpfpyfltliarpvfspvhhtlr 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 FALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 d--qgialalaesytlskdhkvytfklrpsvwsdgtpltaydfeksikqlyfeefspsih 139
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                                                                                                                                                                                                                                                                                                                                             QASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFR 527
                                                                                                                                                                                                                                                                                                                                                                           iatggwiaeyvspvaflsilgnprdltqw--rnsdyektleklylphaykenlkraemi-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esykkgtppstyisngpfvlkkhxhqnylileknphyydhesvkldrvtlkiipdastat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 33.9%; Pr
77; Conservative 105;
                                                                                                                                                                                                                                                                                                             ieeetpiiplyhgkyiyaihpkiqntfgsllghtdlk 528
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.5%;
                                                                                                                                                                                                                           529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 753.5;
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Mismatches 217; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 534;
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Chlamydia trachomatis

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δÃ
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Best Local
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482 ELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFR 527
                                             424
                                                             428 SLATGGWFADFMAFLTIFAYPSGVPPYAINHKDFLEI-----LQNIEQEQDHQKRS 481
                                                                                             366 l--sqedlekitliypiesvclravvqeirqqlfdvlgfkistlgleyhcfldkrsrgef
                                                                                                                                368 LQITAKDLEHLNLIFFVSSSASSLLVQLIREQWKESLGFAIFIVGKEFALLQADLSSGNF 427
                                                                                                                                                                309 talslainretllk--lagkgcsatsfvhpqlsqipattlsq-derialakgyltealkt 365
                                                                                                                                                                                                  308 EALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEE 367
                                                                                                                                                                                                                                                                                                                                                            194
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                                                                                                                                                                                                                                   250 mqlfqknhidlvglpwsssfsleeqrnl-preklfdypvlscsvlfcnihqtplnnpslr 308
                                                                                                                                                                                                                                                                       248 AKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLR 307
                                                                                                                                                                                                                                                                                                        190 yykdkrnkrvfpmisngpfaiqcyepqryllinknplyhakhdvllnsvclqivpdihta 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 853; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                          130 slaliknshavltgalpvedlgvralnaksleivlenpfpyfleilahpvfypvhtslre 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-371125/31
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                                                                                                                                                                                                                                                                                                                                                                                                              134 ALNPIKNVRKIQEGHLSIDHFGVHSPNESTLYVTLESPTSHFLKLLALPVFFPVHKSQRT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-1998;
28-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               72 aa--fqlalaeryhqsddgcvytfflkntfwsngdvvtaydfeesikgiyfreidnpslr 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 LSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWKQVATQEVSGTYAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 vslafgltscyhqkee--pkdvlriaichdpmsldprqvflskdvsivkalyeglvreke 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                           slatgnwiadyhqasaflsvlg-----ngtrykdfqlinwqnqkytnivaqllliqess
                                                                                                                                                                                                                                                                                                                                        L----QSKSLP-TASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529 AA;
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97FR-0015041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
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Pred. No. 5.8e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 226;
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                                                                                                 423
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Дb QYDb Qy Вb

83

127 waldpnnesqyayqlyyikgaeaantgkgslddvavkavndktlkvelnnptpyftelta 121 QVATQEVSGIYAFALNPIKNVRKTQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLA 180

186

ΔÃ

10 ITILLSLSVVLQGCKESSHSSTSRGE------LAINIRDEPRSLDPRQVRLLSEISLV

Conservative 107; Mismatches 249;

Indels Length 544;

25;

Gaps

13;

61

22.5%; Score 617.5; DB 21; 29.4%; Pred. No. 3.3e-47;

8 vtlmliftlvlsacgfggsgsngegkkdskgkttlniniktepfslhpglandsvsggvi 67

rqtfegltr-inadgepeegmaskietskdgktytftirdgvkwsngdpvtaqdfeyawk 126 KHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAF-WSNGDPLTAEDFIESWK 120 Matches Query Match

Local Similarity

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RESULT
AAY97040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
                    than the wild-type strain. Therefore, gram-positive microorganims, especially Bacillus strains, containing a mutation in at least one of the genes of the opp operon can be used for heterologous protein production, especially hormones, enzymes (preferably proteases such as subtilisin), growth factors or cytokines.
Sequence
                                                                                           The opp operon of Bacillus (also known as spook operon) encodes an oligopeptide permease that is required for the initiation of sporulation and the development of genetic competence. The opp operon is a member of the family of ATP-binding cassette (ABC) transporters involved in the import or export of oligopeptides from 3-5 amino acids. Bacillus strains containing a mutation in the opp operon produce more recombinant protein
                                                                                                                                                                                                                                  Production of proteins, such as hormones, enzymes, growth factors or cytokines, in gram-positive microorganisms containing a mutation in a least one of the genes of the opp operon gene cluster
                                                                                                                                                                                                           Disclosure; Fig 1A-M; 32pp; English.
                                                                                                                                                                                                                                                                                                        N-PSDB; AAA51864.
                                                                                                                                                                                                                                                                                                                      WPI; 2000-452412/39.
                                                                                                                                                                                                                                                                                                                                                     Diaz-Torres M,
                                                                                                                                                                                                                                                                                                                                                                               (FERR/) FERRARI E.
                                                                                                                                                                                                                                                                                                                                                                                                                                             24-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Opp operon; SpoOK; oligopeptide permease; sporulation; ABC transporter; ATP-binding cassette transporter; mutation; protein production; oppA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. subtilis oppA ligand binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                              (GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200039323-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oppB; oppC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY97040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY97040 standard; Protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                   (DIAZ/)
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544 AA;
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                                        AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g., eye paratrachoma, and inclusion conjunctivitis; genital diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as convention conjunctivitis; genital diseases such as
nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding i and venereal lymphogranulomatosis. The polypeptides of the in
                                                                                                                                                                                                                                                                                                                                            04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                             Disclosure; Page 836; 1755pp; English.
                                                                                                                                                                                                                                                  WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                 Griffais
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7004
                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPVFFPVHKSQRTLQSKSLPIASGAFYPKN--IKQKQW-----IKLSKNPHYYNQSQVET
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                                                                                                                                                                                                           sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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97FR-0015041.
97FR-0016034.
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   the invention
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AAY20067
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Best Local Similarity
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                                                                                                                                                                                            20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                          Claim
                                                                                            New isolated Borrelia burgdorferi nucleic acids products for the diagnosis, prevention and treat
                                                                                         caused by
                                                                                                                                                                   (HUMA-)
                                                                                                                            N-PSDB;
                                                                                                                                                    Choi GH,
                                                                                                                                                                                                                                                       30-DEC-1998
                                                                                                                                                                                                                                                                       W09859071-A1
                                                                                                                                                                                                                                                                                                   Antigenic protein; vaccine; Lyme disease; infection; detection
                                                                                                                                                                                                                                                                                                                      B. burgdorferi antigenic protein,
                                                                                                                                                                                                                     03-SEP-1997;
                                                                                                                                                                                                                                                                                     Borrelia burgdorferi
                                                                                                                                                                                                                                      18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                    193
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                                                                                                                                  1999-189980/16
                                                                        12; Page 182;
                                                                                                                                                                                                                                                                                                                                                                                                                nklsfvrlhpsglvdmryakns 214
                                                                                                                                                                                                                                                                                                                                                                                                                          KKLSNLGVSPTGVVDFRYAKEN 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFLTIFAY 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                skgvkpyalqdpqfdqlilsieteknpqkrsaliseaslylerqnvieplyhdvfhyttn
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIEPIYHDAFQFAMN 510
                                                                                                                           AAX61764
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                                                                                                                                                                   MEDIMMUNE INC
                                                                                                                                                                            HUMAN GENOME SCI INC
                                                                                         Borrelia,
                                                                                                                                                  Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.0%;
milarity 48.5%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                            97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                                                                                                                     98WO-US12718
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                                                                     275pp; English.
                                                                                      particularly Lyme
                                                                                                                                                  Hanson MS,
                                                                                            prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                        512 AA
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1; Mismatches
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                                                                                                                                                 Lathigra
                                                                                                                                                                                                                                                                                                                      t606.aa
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                                                                                             to develop
diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 192
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This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in infection caused by a member of the Borrelia genus. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can al

of

be used for detection of members

of the Borrelia

genus.

SS

Sequence

512

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RESULT 1
AAY20066
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Best Local Similarity
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                                                                     03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
      Choi GH,
                               (HUMA-)
                                                                                                                                     18-JUN-1998;
                                                                                                                                                                30-DEC-1998
                                                                                                                                                                                          W09859071-A1
                                                                                                                                                                                                                                   Antigenic protein; vaccine; Lyme disease; infection; detection
                                                                                                                                                                                                                                                                B. burgdorferi antigenic protein, f606.aa
                                                                                                                                                                                                               Borrelia burgdorferi
                                                                                                                                                                                                                                                                                               19-JUL-1999
                                                                                                                                                                                                                                                                                                                            AAY20066;
                                                                                                                                                                                                                                                                                                                                                AAY20066 standard; Protein; 529
                                                                                                                                                                                                                                                                                                                                                                                                                                              497
                                                                                                                                                                                                                                                                                                                                                                                                                 473 iapiy 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 pltflsift--qgytqfsshnysnpeynelikksdleldpikrqdilrqaeeiiiekdfp 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 PMAFLTIFAYPSGVPPYA---INHKDFLEILQNIEQEQDHQKRSELVSQA-SLYLETFHI 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 lkyntneankkicefiqngwkknlnidveleneewttylntkangnyeiaragwigdyad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFAD 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iraidektleitlespkpyfidmlvhqsfipv--pvhvtekygqnwtspenmvtsgpfkl 192
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                                         HUMAN GENOME SCI INC
                            MEDIMMUNE INC.
    Erwin AL,
                                                                                                                                                                                                                                                                                            (first entry)
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                                                                  97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                   98WO-US12718
 Hanson MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.5%; Score 505.5; DB 20; Length 512; 28.0%; Pred. No. 4.7e-37;
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Lathigra
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XX DE XX DE

13-SEP-1999

(first entry)

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

Chlamydia pneumoniae lipoprotein sequence.

AAY34798 RESULT

AAY34798 standard; Protein; 448

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
 490
                                                          432 pltflsift--qgytqfsshnysnpeynelikksdleldpikrqdilrqaeeiiiekdfp
                                 497 IEPIY 501
                                                                                                         441
                                                                                                                               372 lkyntneankkicefiqnqwkknlnidveleneewttylntkangnyeiaragwigdyad
                                                                                                                                                                 385 ----SSSASSLLVQLIREQWKESLGFATPIVGKEFALLQADLSSGNFSLATGGWFADFAD 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 181-182; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids - used to devel products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                              325 ttptrratpnfssy
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                                                                                                                                                                                                                                                                                                              269 QETLSNLQSKGHLHSFDYAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                     152 iraidektleitlespkpyfidmlvhqsfipv--pvhvtekygqnwtspenmvtsgpfkl 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 VHSPNESTLVVTLESPTSHFLKLLA----LPVFFPVHKSQRTLQSKSLP---IASGAFYP 208
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                                                                                            PMAFLTIFAYPSGYPPYA---INHKDFLEILQNIEQEQDHQKRSELVSQA-SLYLETFHI 496
                                                                                                                                                                                                                                                                                                                                                keripnekyvfeknnkyydsneveleeitfyttndsstaykmyeneeld---aifgs-ip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLKSAF-WSNGDPLTAEDFIESWKQVATQEVSGIYA-FALNPIKNVRKIQEGHLSIDHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109; Mismatches 197;
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                                                                                                                                                                                                     ---syakslelfnpeiaktllaeagypngn-gfpilk 371
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in nucleotides sequences can also be used as immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
               427
                                           327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae
                                                                                                                    307 REALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALE 366
                                                                                                                                                229 aihllnrgkvdwvgqpwhqgipwel~-hkqsqyhyytypvegafwlclntksphlndlqn
                                                                                                                                                                            247 AAKLFNQGKLNWQGDPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNNKL 306
                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                      187 VHKSQRTLQSKSLÞIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANT 246
                                                                                                                                                                                                                                                                                   129
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21-NOV-1997;
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FSLATGGWFADFADPMAFLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQ 486
                             --qkpltpqeklvltypsdilrcqriaeilkeqwk-aagidlilegleyhlfvnkrkvqd
                                                         ELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGN
                                                                                          rhrlatcidkrsiieealggtggpaetl--
                                                                                                                                                                                                          ifkpenp-klfsgpytlveyfpghn-----ihlkknpnyydyhcvsinsiklliipdiyt 228
                                                                                                                                                                                                                                                                    ---yaqensp-----hiqifqglnfstpssnaitihldspnpdfpkllafpa-fa 174
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                                                                                                                                                                                                                                                                                                 SGIYAFALNPIKNVRKIQEGHLSI-DHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFP 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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97FR-0014673.
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27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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Pred. No. 4.7e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       190;
                                                                                          -srgapqpnqykk-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 448;
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                                                            426
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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          115 FIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSH
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Pred. No. 2e-32;
11; Mismatches 25
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               The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic
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the present invention can also be used
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AAY19870
                                                                                                                                                                                                                                                                                                                                    RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 138;
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Best Local
                       03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                       18-JUN-1998;
                                                                                                                   30-DEC-1998.
                                                                                                                                            W09859071-A1
                                                                                                                                                                       Borrelia burgdorferi
                                                                                                                                                                                           Antigenic protein; vaccine; Lyme disease;
                                                                                                                                                                                                                      B. burgdorferi antigenic protein,
                                                                                                                                                                                                                                                                                                     AAY19870 standard; Protein;
                                                                                                                                                                                                                                                     19-JUL-1999
                                                                                                                                                                                                                                                                               AAY19870;
                                                                                                                                                                                                                                                                                                                                                                            472
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                                                                                                                                                                                                                                                                                                                                                                                             478 QKRSELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 KLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKLFKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 ginlyqvneldl-----vringqyvqqyqddpgyvshpdva-nyfldfnkkegtplanv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ldsvknsfeirngeksvdelgisapndkefivelkqaqpsflavvsiawlapqnqkfvea 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 GNIEPALAEDYSLSSDGLTYTFKLKSAF-WSNGDPLTAEDFIESWKQVATQEVSGIYAFA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 GCKESSHSSTSRGELA----INIRDEP--RSLDPRQVRLLSEISLVKHIYEGLVQENNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 gtkeaaekvds-gnlaaeqkisisspapistldttqttdkntftmaqhlfeglyrfddds
                                                                                                                                                                                                                                                                                                                                                                   kqfaeykeaedilinqdaaqvplyqsasnylinpklkgi 510
                                                                                                                                                                                                                                                                                                                                                                                                                     rreknyelslsgwiagsseldsyfnlyagessy-nygnyhnakydqlveeartinannpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt qaewtkaqadvgkkvklsllaadtdqgkriaeyvqsqlqenlpgleitissqpsnnvnqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEELQITAKDL-EHLNL-IFPVSSSASSLLVQLIREQWKESL-GFAIPIVGKEFALLQAD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                LSSGNFSLATGGWFADFAAFLTIFAYPSGVPPYAINHK----DFLEILQNIEQEQDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAKLFNQGKLNWQGPPWGERIPQETLSNLQ-SKGHLHSFDVAGTSWLTFNINK-FPLNNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qgkdyaldsehllysgpftlanwdatsdtw-tlkknpeyydadqvkleevavstikednt
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                                                                                                                                                                                                                                                  (first entry)
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                                   97US-0057483.
97US-0050359.
97US-0053344.
                                                                                       98WO-US12718.
                      97US-0053377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 452.5; DB 20; 26.6%; Pred. No. 3.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identify agonists and antagonists
                                                                                                                                                                                                                                                                                                      523
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                                                                                                                                                                                                                       f607.aa
                                                                                                                                                                                         infection; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244; Indels
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(HUMA-) HUMAN

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RESULT 15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                              19-JUL-1999
                                                                             AAY19871;
                                                                                                             AAY19871
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                                                                                                                                                                                                                      462 KDFLEILQNIEQEQDHQKRSELVSQA-SLYLETFHIIEPIY 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 97-98; 275pp; English.
                                                                                                                                                                                                 450
                                                                                                                                                                                                                                                    390 Ininleieneewttflgsrrtgnyqmssvgwigdyfdpltfldslfttenhflgaykysn 449
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                                                                                                                                                                                                                                                                                                                                                                     344
                                                                                                                                                                                                                                                                                                                                                                                         287 afnttikpldnlkvrqaislaidretltkvvlkgssdptrnltpkfddysygknlilfdp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 KTITIHFIPDANTAAKLFNQGKLNW-QGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRKISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISL
                                                                                                                                                                                    keydalikksnfeldpikrqdilrqaeeiiaekdfpmaply 490
                                                                                                                                                                                                                                                                                      LGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFL-TIFAYPSG-VPPYAINH 461
                                                                                                                                                                                                                                                                                                                       enakkllaeagypdgkgfp-------tlkykisegrpt-taeflqeqfkki
                                                                                                                                                                                                                                                                                                                                                     EHQKQEMAQRQAYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKES 403
                                                                                                                                                                                                                                                                                                                                                                                                                          TFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPT-NIHSY------P
                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev-ifyptegsvaynmyingeldflqg-----aeknnleeikirddyysglkngmayi 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lrilnkk taamyan likstik naqeyf detvpe selgikaidsk tleitlt spkpyfpdm\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQVATQEVSGIYAFAL-NPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LALPVFFPV--HKSQRTLQSKSLP---IASGAFYPKNIKQKQWIKLSKNPHYYNQSQVET 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lthsayipvpmhivekygenwtnpenivvsgayklkersindkivieknekyynaknvei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 itnlflglavkdsqtgkykpglakswnisedgiiytfnlredivwsdgvaitaeeikksy 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLK-SAFWSNGDPLTAEDFIESW 119
                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.5%; Score 425.5; DB 20; Length ilarity 23.4%; Pred. No. 9.2e-30; Conservative 131; Mismatches 217; Indels
                                        (first entry)
                                                                                                        Protein; 506 AA
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    used to develop
ment of diseases

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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
              356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                               386 SSASSLLYQLIREQWKESLGFAIPTYGKEFALLQADLSSGNFSLATGGWFADFADPMAFL 445
                                                                                                 335 LPT-NIHSY-----PEHQKQEMAQRQAYAKKLFKEALEELQITAKDLEHLNLIFPYS 385
                                                                                                                                                                                                    199 kivieknekyynaknveldev-ifyptegsvaynmyingeldflqg-----aeknnlee 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 98; 275pp; English
                                                                                                                                    252 ikirddyysglkngmayiafnttikpldnlkvrqaislaidretltkvvlkgssdptrnl
                                                                                                                                                                                                                                                                       139 sktleitltspkpyfpdmlthsayipvpmhivekygenwtnpenivvsgayklkersind 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi GH,
                                                                                                                                                                                                                                      216 WIKLSKNPHYYNQSQVETKTIT1HFIPDANTAAKLFNQGKLNW-QGPPWGERIPQETLSN 274
                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                           102 AFWSNGDPLTAEDFIESWKQVATQEVSGIYAFAL-NPIKNVRKIQEGHLSIDHFGVHSPN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX61568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi
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                                                                                                                                                                                                                                                                                                                                         79 ivwsdgvaitaeeikksylrilnkktaamyanlikstiknaqeyfdetvpeselgikaid 138
                                                                                                                                                                                                                                                                                                                                                                                                                                            43 EPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLK-S 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
egrpt-taeflqeqfkkilninleieneewttflgsrrtgnyqmssvgwigdyfdpltfl
                                                                   tpkfddysygknlilfdpenakkllaeagypdgkgfp---
                                                                                                                                                                    LQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHL
                                                                                                                                                                                                                                                                                                         ESTLVVTLESPTSHFLKLLALPVFFPV--HKSQRTLQSKSLP---IASGAFYPKNIKQKQ 215
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| US-08-961-083-86 | US-08-930-996A-8 | US-U8-856-253-6 | PCT-US91-07035-4 | US-09-105-697-10 | US-08-458-819-4 | US-07-977-434-4 | US-09-184-445-4 | US-09-060-836-4 | US-08-751-189-4 | US-09-061-709-2 | US-08-845-528C-7 | US-08-993-118-7 | US-08-915-136-6 | US-08-405-496A-6 | US-08-480-604A-6 | US-09-264-604-2 | US-08-642-846-2 |
| 86, | Sequence 8, Appli | Sequence 6, Appli | Sequence 4, Appli | Sequence 10, Appl | 4. | | 4 | 4 | Sequence 4, Appli | 2 | 7, | | | 9 | σ. | 2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1 US-08-245-511-48 Sequence 48, Application US/08245511 Patent No. 5928900 APPLICATION NUMBER: US 08/116,: PILING DATE: 01-SEP-1994 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1. TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800 TELEPAX: 201 343-1684 TELEX: 133521 INFORMATION FOR SEQ ID NO: MOLECULE TYPE: HYPOTHETICAL: N ANTI-SENSE: NO IMMEDIATE SOURCE: CLONE: amiA ORIGINAL SOURCE: ORGANISM: Streptococcus pneumoniae COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 642 amino acid CLASSIFICATION: 424 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Masure, H Robert APPLICANT: Pearce, Barbara J APPLICANT: Tuomanen, Elaine TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON NUMBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS: LENGTH: 642 amino acids TYPE: amino acid TOPOLOGY: APPLICATION NUMBER: FILING DATE: 18-MAN COUNTRY: STREET: ADDRESSEE: INFORMATION: Hackensack 07603 New Jersey 411 Hackensack Avenue USA unknown Klauber & Jackson NO peptide 18-MAY-1994 US 08/116,541 US/08/245,511 600-1-069 CIP

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                                                                                                                  Sequence 48, Application US/08600993A
Patent No. 5981229
                                                                                                    GENERAL INFORMATION:
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                 TITLE OF INVENTION:
                                                    APPLICANT: APPLICANT:
   NUMBER OF SEQUENCES:
                                                                                 APPLICANT:
                                                                                                                                                                                                           574 AAPVLSRIVPFTGASAQTGSKGSDVYFKYLK 604
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AUTHORS: Alloing, et al.
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                                                                                                                                                                                                                                                                                                                                                                                                       407 KKALEADGYQFP-IHLDVPVDQASKNYISRIQSFKQSVETVLGVENVVVDIQQMTSDEFL 465
                                                                                                                                                                                                                                                                                                                                                                                                                                        365 LEELQITAKDLEHLNLIFPVSSSASSLL--VQLIREQWKESLGFAIPIV-----GKEF- 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 Y-LAENSVKGLADYLSGTSTDESTYGVKAVDDYTLQYTLNQPEPFWNSKLTYSIFWPLNE 178
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JOURNAL:
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                                             Tuomanen,
                                                                              Masure, H Robert
                                                                Pearce, Barbara J
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BACTERIAL EXPORTED PROTEINS AND
ACELULAR VACCINES BASED THEREON
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IMMEDIATE SOURCE:
                                                                                                   120 Y-LAENSYKGLADYLSGTSTDFSTYGYKAYDDYTLQYTLNQPEPFWNSKLTYSIFWPLNE
                                                                                                                                                                      131 YAFALNPIKNVRKIQEG-HLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/245,511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                        60 NLAPAVAEDWEVSKDGLTYTYKIRKGVKWFTSDGEEYAEVTAKDFVNGLKHAADKKSEAM 119
                                                                                                                                                                                                                                                                                                          77 NIEPALAEDYSLSSDGLTYTFKLKSA---FWSNGD---PLTAEDFIESWKQVATQEVSGI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 VLQGCKESSHSSTSRGELAIN--IRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: ZU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGES: 633-644
DATE: 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 18-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 600-1-069 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/600,993A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                    VLAAC-SSSKSSDSSAPKAYGYYYTADPETLDYLISRKNSTTVVTSNGIDGLFTNDNY-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 104; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol
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411 Hackensack Avenue
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 280.5; DB 2;
21.7%; Pred. No. 6.1e-18;
1^4 Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the reference contains a sequence error; the correct sequence shown below is obtained from GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 08/116,541
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                                                                                                           178
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RESULT 3
US-08-245-511-47
                                INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
                                                                                                                                                                                                                                FILING DATE: 01-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 AAPVLSRIVPFTGASAQTGSKGSDVYFKYLK 604
                                                                                                    TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 KKALEADGYQFP-IHLDYPYDQASKNYISRIQSFKQSVETYLGVENYVYDIQQMTSDEFL 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 LEELQITAKDLEHLNLIFPVSSSASSLL--VQLIREQWKESLGFAIPIV------GKEF- 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 LAVRNLEVKPDEVSAGEKTEGDLVAAQLPAYGDEWKGVNLADGQDGLENADKAKAEERKA 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                Sequence 47, Application US/08600993A Patent No. 5981229
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                     566 IP
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                      COUNTRY:
ZIP: 0760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 NLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTI--FLGRAKTA 331
                                                         STATE:
                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 DGQDTSKPAENFKDGSLT-----AARLYPTSASFAELEKSMKDNIVYTQQDSITYLVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 FALNPIKNVRKIQEGHL-SIDHFGYHSPNESTLVVTLESPTSHFLKLLALPVFFPYHKSQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VPSMAEDWSVSKDGLTYTYTIRKDAKWYTSEGEEYAAVKAQDFVTGLKYAADKKSDALYP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 VLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSGNI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 EPALAEDYSLSSDGLTYTFKL-KSAFW--SNGD---PLTAEDFIESWKQVATQEVSGIYA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VLAACSGSGSSAKGEKTFSYTYETDPDNLNYLTTAKAATANITSNVVDGLL-ENDRYGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TIFAYPSG----VPPYAINHKDFLEILQNI-EQEQDHQKRSELVSQASLYLETFHII 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLQKDEVNNITYFAENAAGEDW-----DLSD-----NVGWGPDFADPSTYLDIIKPSYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KSALQAEGVTFP----IHLDMFVDQTATTKVQRVQSMKQSLEATLGADNVIIDIQ 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt RNLFVPPTFVQADGKNFGDMVKEKLVTYGDEWKDVNLADSQDGLYNPEKAKAEFAKA----}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFLNSKGDDFAKATDPSSLLYNGPYLLKSIYTKSSYEFAKNPNYWDKDNVHIDKVKLSFW 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTLOSK------SLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VQESIKGLDAYVKGEIKDFSQVGIKALDEQTVQYTLNKPESFWNSKTTMGVLAPV--NE 177
                                                                        Hackensack
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                                                     New Jersey
                                                                                    411 Hackensack Avenue
                                                                                                                                                                                                              Masure, H Robert
Pearce, Barbara J
Tuomanen, Elaine
                                         USA
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                                                                                                               Klauber & Jackson
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                                                                                                                                                                    BACTERIAL EXPORTED PROTEINS AND ACCLLULAR VACCINES BASED THEREON
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Pred. No. 5.4e-17;
d; Mismatches 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
446 ----TIFAYPSG---VPPYAINHKDFLEILQNI-EQEQDHQKRSELVSQASLYLETFHII 497
                                    457 QLQKDEVNNITYFAENAAGEDW~----DLSD-----NVGWGPDFADPSTYLDIIKPSVG 505
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                            357 AKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLL--VQLIREQWKESLG------
                                                                                                                                                                                                                                                                          292
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APPLICATION NUMBER: US 08/116,541
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                                                                                                                                                                                                                                 332 DHLL--PTNIHS-----
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 21.6%; Pres 130; Conservative 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/245,511 FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/600,993A FILING DATE: 1-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VLAACSGSGSSAKGEKTFSYIYETDPDNLNYLTTAKAATANITSNVVDGLL-ENDRYGNF 60
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COMPUTER: I
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                                                                                                          ----KSALQAEGVTFP----IHLDMPVDQTATTKVQRVQSMKQSLEATLGADNVIIDIQ 456
                                                                                                                                                                                   RNLFVPPTFVQADGKNFGDMVKEKLVTYGDEWKDVNLADSQDGLYNPEKAKAEFAKA--- 405
                                                                                                                                                                                                                                                                                                 NLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTI--FLGRAKTA 331
                                                                                                                                                                                                                                                                                                                                     DGQDTSKPAENFKDGSLT-----AARLYPTSASFAELEKSMKDNIVYTQQDSITYLVGT
                                                                                                                                                                                                                                                                                                                                                                                                               EFLNSKGDDFAKATDPSSLLYNGPYLLKSIVTKSSVEFAKNPNYWDKDNVHIDKVKLSFW 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTLQSK-----SLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTITIHFI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FALNPIKNVRKIQEGHL-SIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQ 191
                                                                                                                                                                                                                                                            NIDRQSYKYT---SKTSDEQKASTKKALLNKDFRQAIAFGFDRTAYASQLNGQTGASKIL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VQESIKGLDAYVKGEIKDFSQVGIKALDEQTVQYTLNKPESFWNSKTTMGVLAPV--NE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPALAEDYSLSSDGLTYTFKL-KSAFW--SNGD---PLTAEDFIESWKQVATQEVSGIYA 132
                                                                                                                                                                                                                                                                                                                                                                                    --PDANTAAKLFNQGKLNWQGPPWGERI------
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                                                                           ---FAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFL-----
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Pred. No. 5.4e-17;
11; Mismatches 214;
                                                                                                                                                                                                                           ----YPEHQKQEMAQRQAY 356
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Best Local
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09385028
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kwamena
APPLICANT: Ashish S
TITLE OF INVENTION:
139 HLLGTEXGGPWREPDADGPVTLETPDERTLVFRLREPFAGMDLLATMPSTTPVPRDRDTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 333000 TELEX: RCA 248593 IDEA UR
                                                                                                                                                                 34 GELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSG----NIEPALAEDYSLS
                                                                                                                                                                                                                            Local
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: D. Douglas Price
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
COMPUTER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                              S-DGLTYTFKLKSAF-WSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEG 147
                                                                                                                                 GTLRLVRTDDFDSLDPGNTYYAYTWNFLRLIGRTLVTFDTAPGKAGQRLVPDLAESLGES 88
                                                               SEDGRVWTYRLREGLRYEDGTPVVSADI----KHAIARSNYGTDVLGAGP-----TYFR 138
                                        HLSIDHFG--
                                                                                                                                                                                                           97;
                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: JACOBSON, PRICE, HOLMAN & STERN, PPLC
The Jenifer Buliding, 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Susan E. Jensen
Kwamena A Aidoo
Ashish S. Paradkar
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24,514
                                 -VHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRT- 193
                                                                                                                                                                                                         74;
                                                                                                                                                                                                                       Score 165.5; DB 4;
Pred. No. 4.2e-07;
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                       212;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                     Length 556;
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; ORGANISM: Kurthia sp
US-08-935-263-12
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US-08-935-263-12
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/935,263A CURRENT FILING DATE: 1997-09-22 EARLIER APPLICATION NUMBER: EP 96115540.5 EARLIER FILING DATE: 1996-09-27 NUMBER OF SEQ ID NOS: 23 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Furuichi, Yasuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: Biotin Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                         121 GIISTLLSRNDIIYSDKLNHASIYDGALLSRAKHLRYRHNDLDHLEALLKKSSMEARKLI 180
                                                                                                                                                                                                                                                                                                    356 ------YAKKLFKEAL------EELQITAKDLEHLNLIFPVSS-SASSLL 392
                                                                                                                                                                                                                                                                                                                                                                                     316 -- KEALVSTIF-LGRAKTADHLLPTNIHSYPEHQKQEMA-----QRQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 QGPPWGERIPQET--LSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALD- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 NYHCRRAVQFATDKAAMQEA--YGGAVGGDIATTLLPPTLDGYKHFDRYPYG-----
                                                                                                                                                                                                                                                                                                                                               64 RLKKAMVDAVHTYGAGATASRLI---IGNHPLYEQAEQALVNWKKAEAGLIINSGYNANL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 NMKLREALASALDKEALVSTIFLGRAKTAD---HLLPTNIHSYPEHQKQEMAQRQAYAKK 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QLPCWEEKIKKELAYLEEISQKRELVSTEFAEQPWLM--INGCKMLNLASNNYLGYAGDE 63
                                          NIEQEQDHQKRSELYSQASLYLET-----FHI-----IEPIY----HDAFQFAMNKKLS 514
                                                                                   IDIQMGTFSKALGSFGAYYVGKKWLIDYLKNR--MRGFIYSTALPPAILGAMKTAIELVQ
                                                                                                                                                                      VTDTVFSMDGDFAYLEDLVRLKERYNAMLMTDEAHGSGIYGKNGEGYA----GHLHLQNK 236
----QEPERRSLLQTHSEHFREELTYYGFNICGSRSQIVPIVIGENEKAMEFA--TRLQ 347
                                                                                                                           ADLSSGNFSLATGG------WFADFADPMAFLTIFAYPSGVPPYAIN-HKDFLEILQ
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                                                                                                                                                                                                                 -KESLGFAIPIVGKEFALLQ 419
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; TOPOLOGY: line
; MOLECULE TYPE: p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 3.9%; Score 107; DB 1; Length 1089; Best Local Similarity 18.6%; Pred. No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEFAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 20-JAN-1995 ATTORNEY/AGENT INFORMATION:
      366 EKDSNVNSKNINLFFTDLEMADCKDIIDDLSNRYWSSYLDNKATRNRILKFFMETQ-DWS 424
                                                                                                                                                                                                                                                                199 FTTTTATAFIKKFAPLFRDD-DNSWDDLIYDSKLKGALQSLFKNFIDATFARATELHKKV 257
                                                     226 YNQSQVETKTITIHF-----
                                                                                       308 PELEGASNDDLKETASPMITNQILPPN--QRLWENEDTRKFYEILPDISKTVEESQSSKT 365
                                                                                                                                                  189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           52 VRLLSEISLV------KHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 KEGIAAIAV 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                             NKLQREHQKCQIRTGKLRDEYVEEY-----DKLLPIFIRFKTS----AITLGEFFKLEI 307
                                                                                                                                                                                                                                                                                                        ----KSAFWSNGDPLTAEDFIESWKQV-----ATQE-----VSGIYAFALNPIKNV 141
                                                                                                                                         -----KSQRTLQSKSLPIASGAFYPKNIKQKQW------
                                                                                                                                                                                                                                RKIQEGHLS----
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VENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
VENTION: THE ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
EQUENCES: 6
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                                                 -ANTAAKLFNQGKLNWQ 259
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| | CATION NUMBER 3 DATE: 27-D PPLICATION DA CATION NUMBER | APPLIC FILING PRIOR AP APPLIC | ·· ·· ·· ·· | |
|------------|--|---|---------------------------------------|--|
| | 02110-2804 READABLE FORM: M TYPE: Floppy disk FIRE: IBM PC compatible FIRE SYSTEM: PC-DOS/MS RE: PatentIn Release APPLICATION DATA: | ZIP: COMPUTER MEDIUM COMPUT! OPERAT SOFTWAN CURRENT | ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ | |
| | ALUKESSE: FISH & KICHARDSON STREET: 225 Franklin Street Suite 3100 CITY: Boston STATE: MA COUNTRY- INA | STREET CITY: STATE: COUNTRY | | |
| | OF SEQUENCES: | NUMBER | | |
| | OF INVENTION: PRODUCT OF INVENTION: PRINCE | TITLE | | |
| | INFORMATION: ANT: UNIVERSI OF INVENTION: | GENERAL APPLI TITLE | | |
| | 6930-2 2, Application PC/TUS9516930 | RESULT 9 PCT-US95-16 ; Sequence | ט פיי | |
| | H 700 | Db 700 | Ы | |
| | H 502 | Qу 502 | 0 | |
| 699 | VIRCIDQVLEN | Db 643 | ь | |
| 501 | EILQNIEQEQDHQKRSELVSQASLYLETFHIIEP | Qy 458 | | |
| 642 | | Db 583 | н | |
| 457 | LLQADLSSGNFSLATGGWFADFADFMAFLTIFAYPSGVPPY | Qy 417 | | |
| 582 | QQFYR | Db 524 | | |
| 416 | FKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFA | Qу 361 | | |
| 523 | FESEMIKFQLIPSFMIFHKIRTLIMYMQVPNNVEILTYLLEHSGKFLLNKPEY | Db 470 | - | |
| 360 | REALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMAQRQAYAKKL | Qy 307 | | |
| 469 | KLPVYSRFIATNSKYMPBIVSEFINYLDNGFRSQLHSNKINVKNI | Db 425 | | |
| 306 | GPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKL | Qy 260 | | |
| 424 | EKDSNVNSKNINLFFTDLEMADCKDIIDDLSNRYWSSYLDNKATRNRILKFFMETQ-DWS | Db 366 | | |
| 259 | YNQSQVETKTITIHFIPDANTAAKLFNQGKLNWQ | Qy 226 | _ | |
| 365 | PELEGASNDDLKETASPMITNQILPPNQRLWENEDTRKFYEILPDISKTVEESQSSKT | Db 308 | | |
| 22! | KSQRTLQSKSLPIASGAFYPKNIKQKQWKSQRTLQSKSLPIASKNPHY | Оу 189 | | |
| 30: | NKLQREHQKCQIRTGKLRDEYVEEYDKLLPIFIRFKTSAITLGEFFKLEI | Db 258 | | |
| 188 | RKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVH- | Qy 142 | | |
| 25 | FTTTIATAFIKKFAPLFRDD-DNSWDDLIYDSKLKGALQSLFKNFIDATFARATELHKKV | Db 199 | | |
|)-1 -4- | KSAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNV | Qy 100 | | |
| | : : : : : : : : : : : : : : | Db 144 | | |
| 99 | ~ H | Оу 52 | | |

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RESULT 10
US-08-328-256-10
; Sequence 10, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
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GENERAL INFORMATION:
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Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acids
STRANDEDNESS: not relevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                 700 H 700
                                                                                                                                                                                            502 H 502
                                                                                                                                                                                                                 643 ---RRDFVIRCIDQVLENIERGLEINDYGQNMHRISNVRYLTEIFNFEMIKSDVLLDTIY 699
                                                                                                                                                                                                                                                       458 AINHKDFL----EILQNIE---QEQDHQKRSELVSQASLYLETFH-----IIEDIY 501
                                                                                                                                                                                                                                                                                                583 LIRSELSSLDFKHIVKLVRKAHWDDVAIQKVLFSLFSKPHKISYQNIPLLTKVLGGLYSY 642
                                                                                                                                                                                                                                                                                                                                                                                                524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 --IFFSEMIKFQLIPSFMIFHKIRTLIMYMQVPNNVEILTVLLEHSGKFLLNKPEY---- 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 REALASALDKEALVSTIFLG----RAKTADHLLPTNIHSYP---EHOKQEMAQRQAYAKKL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 KLPVYSRFIATNSKYMPEIVSEFINYLDNGFRSQLHS------NKINVKNI-- 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 GPPWGER-----IPQETLSNLQS--KGHLHSFDVAGTSWLTFNINKFPLNNMKL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 EKDSNVNSKNINLFFTDLEMADCKDIIDDLSNRYWSSYLDNKATRNRILKFFMETQ-DWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 YNQSQVETKTITIHF-----IPD-----ANTAAKLFNQGKLNWQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 PELEGASNDDLKETASPMITNQILPPN--QRLWENEDTRKFYEILPDISKTVEESQSSKT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 -----KSQRTLQSKSLPIASGAFYPKNIKQKQW------IKLSKNPHY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 NKLQREHOKCQIRTGKLRDEYVEEY-----DKLLPIFIRFKTS----AITLGEFFKLEI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 RKIQEGHLS------IDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVH- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 FTTTIATAFIKKFAPLFRDD-DNSWDDLIYDSKLKGALQSLFKNFIDATFARATELHKKV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 -----KSAFWSNGDPLTAEDFIESWKQV------ATQE-----VSGIYAFALNPIKNV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 LRVFTELYLVGVFRTLDDIESKDAIPNFLQKK--TGRKDPLL---FSILREILNYKFKLG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (UL
TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 VRLLSEISLV------KHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKL- 99
                                                                                                                                                                                                                                                                                                                                           LLQADLSSGNF----SLATGGWFADFADPMAFLTIFAYP------
                                                                                                                                                                                                                                                                                                                                                                               -KELMEKMVQLIKDKKNDRQLNMNMKSALENTITLLYPPSVKSLNVTVKTTTPEQQFYRI 582
                                                                                                                                                                                                                                                                                                                                                                                                                      FKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKE----FA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%; Score 107; DB 5; Length 1089;
milarity 18.6%; Pred. No. 0.46;
Conservative 89; Mismatches 206; Indels 194; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617)542-8906
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-10

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Best Local Similarity 19.3%; Pred. No. 0.26;
Matches 114; Conservative 77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVI
        338 NIR---SLSDSFH-----
                                  303 NMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYP-----EHQKQEMAQRQAY 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                        296
                                                                                                              257 NWQGPPWGERIPQETLSNLQSKG----HLHSFDVAGTSWLTFNINKF------PLN 302
                                                                                                                                                                                                                                                                      172 TSHFLKLLA-----LPVFFPVHKSQRTLQSKSLPIASGAFYPKNIK------
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APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                 196 TTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPP-----PENIEVSVQNQNYVLKW 248
                                                                                                                                                                                                                                                                                                             174 ------KIYKLSPE 195
                                                                                                                                                                                                                                                                                                                                                  112 AEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 IKLSGCQNITSTKCNFSSLKLNVYEETKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VYLQGCKESSHSSTSRGELAINIRDEPR------52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C
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                                                                                                                                                       DYTYANMTFQVQWLHAFLKRNPGNHLYKWKQ-----IPDCENVKTTQCVFPQ--- 295
                                                                                                                                                                                          ------QKQWIK--LSKNP--HYYNQSQVETKTITIHFIPD---ANTAAKLFNQGKL 256
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                                                                         -NVFQKGIYLLRVQASDGNNTSFWSEEI-KFDTEIQAFLLPPVF 337
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-IYIGAPKQSGN-TPV-IQDYPLIYEIIFWENTSNAERKII 385
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                                                                                                                                                                                                                                                                                                                                                                                             --- ISPGTKDSVMWALDGLSFTYSL--LIWKNS---- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 557;
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                                                                                                                                                                                                                                                                            212
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| ad Ao | Que Bes Mat | US-08 II | Db RESU | Qy | Оу | Дb |
|---------------------------------------|--|--|--|------------------------------------|--|------------|
| 18 VVLQGCKESSHSSTSRGELAINIRDEPRSLDPRG | Query Match 3.8%; Score 104.5; DB 1; Length 557; Best Local Similarity 19.3%; Pred. No. 0.26; Matches 114; Conservative 77; Mismatches 150; Indels 251; Gaps 33; | SEQUENCE 2. Application US/08471454 PETENTAL INFORMATION: APPLICANT: MCERSEN, Knud E. APPLICANT: UVER, Gilles APPLICANT: UVER, Gilles APPLICANT: UVERNION: CONA FRAGMENT CODING FOR THE GENE FOR ITILE OF INVENTION: THE ALCHA INVESTERON RECEPTOR AND PROCESS ITILE OF INVENTION: PRECARATION OF THE CORRESPONDING PROTEIN CORRESPONDENCE ADDRESS: ADDRESSEE: MION & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD STATE: VIRGINIA COUNTRY: USA. ITILE OF INVENTION: PRECARATION OF THE CORRESPONDING PROTEIN COMPUTER READABLE FORM: ADDRESSEE: ALDRESSEE: ALDRESS | b 484 EQPLKNLLLSTSEEQIEKCFIIENISTLATVEETNQTDEDHKKYSSQTSQDS : ESULT 11 S-08-471-454-2 | 462KDFLEILQNIEQEQDHQKRSELVSQAS 488 | Qy 417 LLQADLSSGNESLATGGWEADEADPMAFLTIFAYPSGVPPYAINH 461 | 357 386 |
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| Oy 53 BLUSE ISLIKRITEGLIOORNALGOMERALANDYSUSSOLITYPFKLASHANADDIT 11 D1 34 BLANDRAIVIH | 134 HLERENKAVHHYEGILVOENNISENITERJALEDYSIJSSOGITYTEKKASAPSHOPLI 12 AEDDIESWKOVATOEVSGITAFALHEVKISISSOGITYTEKKASAPSHOPLI 134 HLERENKAVHHISPOTKOSVMALDGISFTYSILINKNS |
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US-08-471-453-2

; Sequence 2, Application US/08471453

; Patent No. 5886153
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                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                  APPLICANT: MOGENSEN, K
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, G
APPLICANT: GRESSER, IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR THE TITLE OF INVENTION: THE ALPHA INVERFERON RECEPTOR AND PROCESS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                               484 EQPLKNLLLSTSEEQIEKCFIIENISTIATVEETNQTDEDHKKYSSQTSQDS 535
                                                                                                                                                                                                                                                                                                                       462 ----KDFL------EILQNI------EQEQDHQKRSELVSQAS 488
                                                                                                                                                                                                                                                                                                                                                                                                        417 LLQADLSSGNES---LATGGWEADFADPM-----AFLTIFAY----PSGVPPYAINH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 EKK-----TDVTVPNLKPLT-VYCVKARAHTM----DEKLNKSSVFSDAVCEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 AKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 NIR---SLSDSFH-----IYIGAPKQSGN-TPV-IQDYPLIYEIIFWENTSNAERKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 NMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYP-----EHQKQEMAQRQAY 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 NWQGPPWGERIPQETLSNLQSKG----HLHSFDVAGTSWLTFNINKF------PLN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 DYTYANMTFQVQWLHAFLKRNPGNHLYKWKQ------IPDCENVKTTQCVFPQ--- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 -----OKOMIK--LSKND--HYYNOSQVETKTITIHFIPD---ANTAAKLENOGKL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 TTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPP-----PENIEVSVQNQNYVLKW 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 TSHFLKLLA-----LPVFFPVHKSQRTLQSKSLPIASGAFYPKNIK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AEDFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 HLEAEDKAIVIH------ISPGTKDSVMWALDGLSFTYSL--LIWKNS---- 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 3.8%; Score 104.5; DB 2; Local Similarity 19.3%; Pred. No. 0.26; nes 114; Conservative 77; Mismatches 150;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 VVLQGCKESSHSSTSRGELAINIRDEPR------52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                   -----TKPGNTSKIWLIVGICIALFALPFVIYAAKVFLRCINYVFFPSLKPSSSIDEYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLLSE-ISLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : (703) 816-4100
200797 NIXN UR
                                                                                                 UZE, Gilles
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                                                    Ion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE, DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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338 NIR---SLSDSFH-----IYIGAPKQSGN-TPV-IQDYPLIYEIIFWENTSNAERKII 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                    303 NMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYP-----EHQKQEMAQRQAY 356
                                                                                                                          257
                                                                                                                                                                                      213 ------OKOWIK--LSKNP--HYYNQSQVETKTITIHFIPD---ANTAAKLFNQGKL 256
                                                                                                                                                                                                                               196 TTYCLKVKAALLTSWKIGVYSPYHCIKTTVENELPP-----PENIEVSVQNQNYVLKW 248
                                                                                                                                                                                                                                                                 172 TSHFLKLLA-----LPVFFPVHKSQRTLQSKSLPIASGAFYPKNIK-----
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                                                                                                                                                                                                                                                                                                                                                                                       134 HLEAEDKAIVIH-------ISPGTKDSVMWALDGLSFTYSL--LIWKNS---- 173
                                                                                                                                                        249 DYTYANMTFQVQWLHAFLKRNPGNHLYKWKQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 VVLQGCKESSHSSTSRGELAINIRDEPR-------
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APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
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                                                                                                                NWQGPPWGERIPQETLSNLQSKG----HLHSPDVAGTSWLTFNINKF------PLN 302
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(703) 816-4100
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THOMAS E.
THER: 32,205
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19.3%;
                                                                            -NVFQKGIYLLRVQASDGNNTSFWSEEI-KFDTEIQAFLLPPVF 337
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Pred. No. 0.26;
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| υı | 7 1 | Query Ma Best Loo Matches | SSQUENT SOURCE SERVING SOURCE SERVING SOURCE | | | |
| 53 R | 18 V 74 i | Match Local Es 11 | Sequence 4, Appl; Sequence 4, Appl; Sequence 4, Appl; Patent No. 591944 GENERAL INFORMAD APPLICANT: ME APPLICANT: TITLE OF INVENTIFLE OF INVEN | 462 484 | 417 429 | 357 386 |
| RLLSE | KLS | ch 11; | 14 107-588-4 107-588-4 107-588-4 107-588-4 107-588-4 107-588-4 107-588-4 11-588-4 | EQ : | : E | AKK III EKK |
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| :: \TS | VVLQGCKESSHS: : : : : : : : : : : : : : : : | Cor | **SAB-4** **A APPLICATION NUMBERS CANT: MENURE APPLICATION NUMBERS CANTE FOR EXAMPLE APPLICATION CANTERS APPLICATION TERMACE PARTING SYSTEMACE PATER CANTER APPLICATION NUMBERS CANTER AND NUMBERS CANTER | KDFL | LSS | KEA |
| - KH | SHSS | Match Local Similarity Nes 114; Conserva | 14 307-588-4 ence 4, Application of No. 5919453 ERAL INFORMATION: PPLICANT: MEYER, I PPLICANT: PLAVEC, PPLICANT: PLAVEC, ITLE OF INVENTION: STATE: D.C. ZIP: 3000 K SY CITY: Washington STATE: D.C. ZIP: 20007 DMPUTER READABLE FO COMPUTER: EMP PC COMPUTER: BEM PC COMPUTER: PATENTION UNMBER FILING DATE: 30-M APPLICATION UNMBER FILING DATE: 30-M APPLICATION UNMBER FILING DATE: 31-M APPLICATION UNMBER FILING DATE: 31-M APPLICATION UNMBER TILING DATE: 31-M APPLICATION UNMBER TILING DATE: 31-M TORNEY/AGENT INFORMAME: SAXE, BERTIND APPLICATION UNMBER REFERENCE/DOCKET IN TELEPHONE: (202)67 TELEFAX: (202)672 RMATION FOR SEQ ID OUGNICE CHARACTERIS LENGTH: 557 anding OTYPE: aming acid TOPOLOGY: linear LECULE TYPE: prot- | LST | LLQADLSSGNFS- | TEE |
| YEG | STSF KCNF | vat | UP 14 8-307-888-4 8-307-888-4 8-307-888-4 R-207-848-4 R-207-858-4 | SEE | S SKI | TQI : TDV |
| LVQ | RGELAINIRDE : : : FSSLKLNVYEE | 3. 19. ive | Juence 4, Application US/083075 APPLICANT: MENCE, Francois APPLICANT: MAGUIRE, Deborah APPLICANT: WASHINGTON: RECEPTOR, WINDERSSE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington STATE: D.C. ZIP: 20007 COMPUTER READABLE FORM: WEDING TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PATENTIN Release APPLICATION NUMBER: US/08/38 FILING DATE: 05-DEC-1994 APPLICATION NUMBER: PCT/EP9 FILING DATE: 30-MAR-1993 APPLICATION NUMBER: EP 9240. FILING DATE: 31-MAR-1992 APPLICATION NUMBER: 28/665 REFERENCE/DOCKET NUMBER: 18/655 REFERENCE/DOCKET NUMBER: 28/665 REFERENCE/DOCKET NUMBER: 38/619 TELLEPAN: (202)672-3399 FORMATION FOR SED ID NO: 4: BROULECUE TYPE: protein 307-588-4 | QIE | WLI. | TAK TVP |
| ENN | AIN :- | ₩ œ | Patrick rancois Deborah Ivan Ichael G. MONOCLONAL RECEPTOR, MONOCLONAL RECEPTOR, PY disk compatible PC-DOS/MS-D a Release #1 DATA RECEPS #1 DATA PR-1994 PA-100: 28-665 PA-100: 28-665 PA-100: 28-655 PS-99 PR-1992 PA-100: 28-655 PS-99 PR-1992 PA-100: 28-655 PS-993 PR-1992 PR-1992 PR-1992 PR-1992 PR-1993 | KCF: | TGGI | DLE :-: NLK |
| LSG | IRD : : VYE | s 77; | | EILQNI- :: FIIENIS | WFAI | LTJ- - HTNI |
| ISLVKHIYEGLVQENNLSGNIEPA | EPR- : EIKL | Score Pred. | 588 N N N N N N N N N N N N N N N N N N N | ISIN | LATGGWFADFADPM- | ELQITAKDLEHLNLIFPVSSSASSLLV ; ; ; ;; ;; -TDVTVPNLKPLT-VYCVKARAHTM |
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| LAEDYSLSSDGLTYTFKLKSAFWSNGDPLT: | VVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQV : ; ; ; ; ; ; ; ; ; ; | 557; 251 | ⊢i | | LSSGNFSLATGGWFADFADPAAFLTIFAYPSGVPPYAINH- | AKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFA |
| DPL | SLDPRQV : : QIGPPEV | •• | AGAINST | 488 535 | IDE: | VGK CEK |
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| 119 W 978 G | 920 P | 2 0 | ery Ma | LENGTH: TYPE: P ORGANIS: 9-415-5 | CURRENT A CURRENT F NUMBER OF SOFTWARE: | APPLICANT: TITLE OF IN | sequence o, patent No. GENERAL INF APPLICANT: | T 15 | 484 | 462 | 429 | 417 | 386 | ນ ເມ ກ ເມ | 303 | 296 | 257 | 249 | 213 | 196 | 172 | 174 | 112 | 134 |
| WKQVATQEVSGIYAFALNPIKNYRKIQEGHLSIDHEGYHSPNESTLVVTLESPTSHFL 176 | SL6SDGLT-YTFKEK 118 | NIRDEPRSLDPRQYRLLSEISLVKHIYEGLVQENNLSGNIEPALAEDY 86 | 3.8%; Scor imilarity 20.0%; Pred; Conservative 90; M | LENGTH: 2071 TYPE: PRT TYPE: AST GOSSYPII ORGANISM: AST GOSSYPII | TT APPLICATION NUMBER: US/09/415,522A TT FILING DATE: 1999-10-08 OF SEQ ID NOS: 28 RRE: Patentin Ver. 2.0 | | Applicati 6291660 ORMATION: Gaffney, Wendland | -6 | TIATVEETNQTDEDHKKYSSQTSQDS | | IYAAKVFLRCINYVFFPSLKPSSSIDEYFS | FLTIFAYPSGVPPYAINH | EKKTDVTVPNLKPLT-VYCVKARAHTMDEKLNKSSVFSDAVCEK 428 | NIRSLSDSFHIYIGAPKQSGN-TPV-IQDYPLIYEIIFWENTSNAERKII 385 | REALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHOKQEMAOR | | NWQGPPWGERIPQETLSNLQSKGHLHSEDVAGTSWLTENINKEPLN 302 | : : : 29 | | SVQNQNYVLKW | IASGAFYPKNIK | LSPE 1 | ESP | HLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNS 173 |

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Search completed: July 26, 2002, 04:38:56 Job time: 3864 sec

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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-049-783-1
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-385-028-1 + 165.50
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-462-467B-3 - 117.00
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-334-179A-3 - 117.00
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Database sequences: 383533
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-Q=/Cgn2_1/USPTO_spool/US09824567/runat_23072002_141351_13464/app_query.fasta_1.596
-DB=Issued_patents_NA -QPMT=fastap -SUFFIX=rni -GAPOP=12.000
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Align seg 1/1 to: US-09-381-862-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09381862 Patent No. 6245906
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (312) 474-0448 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Cawley, Jr., Thoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFECTIONS TITLE OF INVENTION: CAUSED BY STREPTOCOCCUS PYOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Matsuhisa, Akio TITLE OF INVENTION: PROBES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cawley, Jr., Thomas A. REGISTRATION NUMBER: 40,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-MAR-1998

    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive/6300 Sears Tower

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abe, Kanako
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                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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                                                                                                    282.00
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58.588
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                                                                                                  Percent Identity: 24.941
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from: 1
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to: 3549
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| 787 | AGAAAAGTAAATGGTTGGCAGCTGTAAGTGTTGCGATCTTGTCAGTATCC 2 | 331 |
|-------------|---|-----------|
| 18 2332 | ValValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerAr 3 :::::: | 381 |
| w | GlyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProA | 0 |
| | AAAACCTACAAGTACGTTTTTGTTAACGATCCAAAATCATTGGATTATA 2 | 431 |
| 50 2432 | rgGinValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGlu 6 :::::: TTTTGACTAATGGCGGTGGAACGACTGATGTTGATAACACAAATGGTTGAT 2 | 6 481 |
| 67 2482 | uValGlnGluAsnAsnLeuSerGlyAsnTleGluProAlaLeuAl 8 | 3 528 |
| 83 2529 | aGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuL 1 :::: ::::: :::: :::: ::: :: :::: | 00 |
| 100 2579 | eTrpSerAsnGlyAspProLeu 1 | 10 628 |
| 111 2629 | rGlnGluVa 1 ::::: CGATAAATC 2 | 27 678 |
| 127 !679 | 1SerGlyIleTyrAlaPhoAlaLeuAsnProIleLysAsnValArgLysI 14 ::::::::: :::: AGATGCTCTTTACGTTGTTGAAGATTCAATAAAAAACTTAAAGGCTT 27 | 14 |
| 144 ?726 | leGlnGluGlyHisLeuSerIleAspHisPheGlyValHisSerProAsn 16 ::: :::::::::::::::::::::::::::: | 50 775 |
| 161 776 | GluSerThrLeuValValThrLeuGluSerProThrSerHisPheLeuLy 17 :::::: :::: | 77 |
| 177 826 | ProValPhePheProValHisL ::: AGTGTGCTTTTCCCAGTT | 169 |
| 194 870 | AAAGATTTTGGTACAACCGATC |)1 |
| 202 920 | oLysa ::: GAGCG | 6,0 |
| 218 970 | SLeuSerLysAsnProHisTyrTyrAsnGinSerGlnValGluThrLysT 23 :::: :::: ::::: ATTCCATAAAAATGAAAACTACTGGGATGCTAAGAATGTTGGGATAGAAT 30 | 19 |
| 235 020 | hrleThrleHisPheIleProAspAlaAsnThrAlaAlaLys 24 :::: :: CTGTTAAATTGACTTACTCAGATGGTTCAGACCCAGGTTCGTTC | 9 |
| 250 070 | LeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyProPr 26 :::::: ::::::::::::::::::::::::: | 2 |
| 262 120 | OTrpGlyGluArglleProGlnGluThrLeuSerAsnLeuGlnSerLysG 27 :::::::::::::::::::::::::::::::::: | 59 |
| 279 160 | e | , U |

| 195 InSerLys |
|---|
| 178 uLeuAlaLeuProValPhePheProValHisLysSerGlnArgThrLeuG 195 :::::: |
| .b2 SerThrLeuValVal ::: ::: 48 CAGACAGTTCAGTAC |
| 46 luGlyHisLeuSe :: :::::::::::::::::::::::::::::::: |
| 29 yIleTyr :::: 51 TCTTTAC |
| 113 GluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValSerGl 129 ::: ::: ::: ::::: 301 CAAGACTTTGTAACAGGACTAAAATATGCTGCTGATAAAAAATCAGATGC 350 |
| 101 erAlaPheTrpSerAsnGlyAspProLeuThrAla 112 :: |
| 85 pTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysS 101 ::: ::: ::: |
| Valo |
| 52 alArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeu 68 :: ::::::::::::::::::::::::::::::::: |
| 5 uLeu |
| 4 9 |
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| ignment_block: S-09-824-567-2 x US-08-245-511-46 |
| ignment_scores: Quality: 270.50 Ratio: 0.902 Gaps: 25 ercent Similarity: 49.834 Percent Identity: 21.595 |
| NAME/KEY: CDS LOCATION: 11932 5-08-245-511-46 |
| IMMEDIATE SOURCE: CLONE: SPRU98 EFACTURE: SPRU98 |
| ENSE: NO AL SOURCE: NISM: Sti |
| TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO |

| 430 | 414 GluPheAlaLeuLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAl | |
|---------------------|---|--|
| 1428 | AAGACGAAGTAAACAATATTACA | |
| ب د | | |
| 05 | 401 sgluserleugly | |
| 401 1328 | 387 SerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLy ::: ::::::::::::::::::::::::::::::: | |
| 386 1278 | 0 leThrAlaLysAspLe :: 1 TGACATTCCCA | |
| 370 1240 | 353 gGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGlnI ::: ::: 1215 TAAATCAGCCTTACAAGCAGAAAGGTG | |
| 353 1214 | 65 CAGGATGGTCTTTACA | |
| 1164 | 15 | |
| 341 | 341 | |
| 341 | 336 oThrAsnIleHisSer | |
| 336 | 24PheLeuGlyArgAlaLySThrAlaAs | |
| 323 | 307 rgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLeuValSerThrIle ::: ::: ::::: ::: ::: 965 GTCAGGCTATTGCCTTTGGTTTTGATCGTACAGCCTATGCCTCTCAGTTG | |
| 307 | 90 rTrpLeuThrPheAsn1 15 CGATGAACAAAAGGCA1 | |
| e 290 914 | 74 ASE 74 AAT | |
| r 273 A 873 | 24 | |
| . 267 G 823 | 4 TCTCTATCCAACAAGTGCAAGTTTCGCAGAGCTTGAGAAGAGTATGAAG | |
| r 266 G 773 | 50 LeuPheAsnGlnGlyLysLeuAsnTrpGlnGlyProl | |
| s 249 : A 741 | hrIleThrIleHisPheIle ::: | |
| T 235 A 691 | 218 SLeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrLys ::::::: ::: ::::::::::: ::: 642 ATTTGCGAAAAATCCGAACTACTGGGATAAGGACAATGTGCAFATTGAC | |
| y 218 : A 641 | 202 AlaSerGlyAlaPheTyrProLysAsnIleLysGlnLysGlnTrpIleLy ::: | |

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seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-600-993A-46
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 2019 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Application US/08600993A Patent No. 5981229
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1696 ATTCCA 1701
                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1646 ATGATAAATACGCTGCAGCCCAAGCTTGGTTGACAGATAGTGCTTTGATT 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1596 AAAATTGGTTACTGAGGCTGGTGATGAGACTACAGATGTTGCTAAACGCT 1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 erGluLeuValSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIle 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 uGluIleLeuGlnAsnIle...GluGlnGluGlnAspHisGlnLysArgS 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 SerGly......ValProProTyrAlaIleAsnHisLysAspPheLe 465
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                                                                 TELEPHONE: 201 343-1684
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                                                                                                                                       REFERENCE/DOCKET NUMBER: 600-1-069
                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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Pearce, Barbara J
Tuomanen, Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klauber & Jackson
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                                                                                                                                                        26,742
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      195 lnSerLys.....
                                  498 GACAACCATGGGTGTGCTTGCGCCAGTT....AATGAAGAGTTTTTGA 541
                                                                              178 uLeuAlaLeuProValPhePheProValHisLysSerGlnArgThrLeuG 195
                                                                                                                       448 CAGACAGTTCAGTACACTTTGAACAAACCAGAAAGCTTCTGGAATTCTAA 497
                                                                                                                                                                                                       398 AAGGGGAAATCAAAGATTTCTCACAAGTAGGAATTAAGGCTCTGGATGAA 447
                                                                                                                                                            162 SerThrLeuValValThrLeuGluSerProThrSerHisPheLeuLysLe 178
                                                                                                                                                                                                                                              146 luGlyHisLeu...SerIleAspHisPheGlyValHisSerProAsnGlu 161
                                                                                                                                                                                                                                                                                        351 TCTTTACCCT...GTTCAAGAATCAATCAAAGGGTTGGATGCCTATGTAA 397
                                                                                                                                                                                                                                                                                                                               129 yIleTyrAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGlnG 146
                                                                                                                                                                                                                                                                                                                                                                          301 CAAGACTTTGTAACAGGACTAAAATATGCTGCTGATAAAAAATCAGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: KU
STRAINE SOURCE:
SPRU98
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                                                                                                                                                                                                                                                                                                                                                                                                                 113 GluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValSerG1 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ATGCAAAATGGTATACTTCTGAAGGTGAAGAATACGCGGCAGTCAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 eralaPheTrp......SerAsnGlyAsp......ProLeuThrala 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 TTGGTCTGTATCCAAGGATGGATTGACTTACACTTATACTATCCGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 CTA...GAAAATGATCGCTACGGGAACTTTGTGCCGTCTATGGCTGAGGA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 pTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLysLeu...LysS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 ValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAs 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 ATTOTCATACATTTATGAGACAGACCCTGATAACCTCAACTATTTGACAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 alargLeuLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 uLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProArgGlnV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 ValLeuGlnGlyCysLysGluSerSerHisSerSerThrSerArgGlyGl 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..1932
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0.902
49.834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 602
Gaps: 25
Percent Identity: 21.595
.....SerLeuProIle 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2019
                                                                                                                                                                                                                                                                                                                                                                               350
                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
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| us-09-824-567-2 x us-09-103-840A-2/rev | alignment_scores: Quality: 176.00 Ratio: 0.649 Percent Similarity: 51.326 Percent Identity: 20.265 | 414 GluPheAlaLeuLeuGlnAlaAspLeuSerSerGlyAsnPheSerLeuAl 430 1429 GACTGG |
|--|--|--|

Align seg 1/1 to reverse of: US-09-103-840A-2 from: 1 to: 4403765

54 uLeuSerGluIleSerLeuValLysHisIleTyrGluGlyLeuValGlnG 71

| 4099120CAGCAACGGTGGGCGCATCATCGATCGGTTGTTCGCCGGCCTGATGTCCT | 4099071 |
|--|----------------|
| 71 luAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAspTyrSer ::: :::::: ::: | 87 4099030 |
| 88 LeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSerAlaPh ::: ::::::::: :::: #1099029ATCGAGAGCGCCGATAACCTCAACTGATCACTGTCAAACCCGGCTG | 103 4098980 |
| 103 eTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGluSerT : :::::::: :::: ::::: ::::: | 119 4098930 |
| 119 rpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheAlaLeu | 135 4098880 |
| 136 ASNPYOTIELYSASNVALARGLYSILEGIngluGl:::: ::::::::::::::::::::::::: | 147 4098830 |
| 147 yHisLeuSerIleAspHisPheglyValHisSerProAsnGluSerThrL :::: | 164 4098786 |
| 164 euValValThrLeuGluSerProThrSerHisPheLeuLysLeuLeuAla :::::: ::::: | 180 4098736 |
| 181 LeuProValPhePheProValHisLysSerGlnArgThrLeuGlnSe | 196 4098686 |
| rLysSerLeuProIleAlaSerGlyAlaPhe | 206 4098636 |
| 207TyrProLysAsnIleLysGlnLysGlnTrpIleLys ::: :::::: | 218 4098598 |
| LeuSerLysAsnProHisTyrTyrAsnGlnSerGlnValGluThrLysTh | 235 4098548 |
| rileThrileHisPheIleProAspAlaAsnThrAlaAlaLysLeuPheA ::: ::::::::::::::: 7TTTGCGATTCGAGTTCTACGCCAATCTGGACACCGCCTATGCCGACTTGC | 252 4098498 |
| <pre>IGLyLySLeuAsnTrpGlnGlyProProTrpGlyGluArg </pre> | 266 4098448 |
| 267 IleProGlnGluThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSe; ::: | 283 4098398 |
| 283 rPheAspValAlaGlyThrSerTrpLeuThrPheAsnIleAsnLysphep 3 ::::: | 300 4098357 |
| 300 roLeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAsp 3 :::::::::::::::::::::::::::::::::::: | 315 1098307 |
| 316 LysGluAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrAla 3 ::: ::: 1098306CGGCCGCAAATCTGCCAGGAGATCTTCGCCGGAACCCGCAGTCCGGCCCG 4 | 331 1098257 |
| 332AspHisLeuLeuProThra 3 | 338 |

| seq_documentation_block: Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION: APPLICANT: FLEISCHAAN, Robert D. APPLICANT: WHITE, Owen R. APPLICANT: WENTER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-2007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 198-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.1 LENGTH: 4411529 TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV US-09-103-840A-1 | _name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09- | 515 nLeuGlyValSerProThrGlyValValAspPhe 526 | 499 ProIleTyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAs 5: | 484 alSerGlnAlaSerLeuTyrLeuGluThrPheHisIleIleGlu 4097801TCAACGACCCGCAGCGAATCCTGTTTCACGACATGCCAGTTGTG 4 | 467 eLeuGlnAsnIleGluGlnGluGlnAspHisGlnLysArgSerGluLeuV 4 | 451 ProSerGlyValProProTyrAlaIleAsnHisLysAspPheLeuGluII 4 ::: :::: 4097901GGCGCCGGATCCAACGACGTCGGCTACATCAACCCGGAATTCGACGCGGC 4 | 435 heAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr 4 ::: ::: | 418 uGlnālaAspLeuSerSerGlyāsnPheSerLeuālaThrGlyGlyTrpp 4 | 402 GluSerLeuGlyPheAlaIlleProIleValGlyLysGluPheAlaLeuLe 4 ::::::::::::::::::::::: | 386 erserAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLys 4 ::: :::::: :::::: 4098068ACAGCATCAAGAACGTGTTGGGCATCGATGGGTGGCCGCGCGCG | 369 nIleThralaLysAspLeuGluHisLeuAsnLeuIlePheProValSerS 3 | 353 ArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGl 3 ::: ::: ::: | 338 snIleHisSerTyrProGluHisGlnLysGlnGluMetAlaGln 3 |
|--|---|--|---|--|--|---|---|--|---|--|--|--|--|
| MYCOBACTERIUM | | | 115 097708 | .98 .097758 | 84 097802 | .67 .097852 | 50 097902 | 35 097952 | .18 .09797 4 | 098019 | 6908601 | 098118 | 352 4098157 |

| Lignment_scores: Quality: 176.00 Ratio: 0.649 Percent Similarity: 51.326 Percent Identity: 20.265 |
|---|
| |
| 9-103-8 |
| 38 IleAsnIleArgAspGluProArgSerLeuAspProArgGlnValArgLe 54 ::: ::: 4106973GTCAACGGCGGAACCGCCCAACCCCCTGATCCCGACCGCCCACCAACGA 4106924 |
| 54 uLeuSerGluIleSerLeuValLysHislleTyrGluGlyLeuValGlng 71 :::::::::::::::::::::::::::::::::::: |
| 71 luAsnAsnLeuSerGlyAsnIleGluProAlaLeuAlaGluAspTyrSer 87 :::::::::::::::::::::::::::::::::::: |
| 88 LeuSerSerAspGlyLeuThrTyrThrPheLysLeuLysSerAlaPh 103 ::: ::: ::: :: ::: |
| 103 eTrpSerAsnGlyAspProLeuThrAlaGluAspPheIleGluSerT 119 : :::::::::::::::::::::::::::::::: |
| 119 rpLysGlnValAlaThrGlnGluValSerGlyIleTyrAlaPheAlaLeu 135 |
| 136 AsnProIleLysAsnValArgLysIle |
| |
| 4 euValVal |
| 181 LeuProValPhePheProValHisLysSerGlnArgThrLeuGlnSe 196 ::: ::: |
| 196 rLysSerLeuProIlealaSerGlyAlaPhe |
| 207TyrProLysAsnIleLysGlnLysGlnTrpIleLys 218 ::: ::::: 4106438cAGCCGGGCCTGGGAACACACACGTCAGAATCGAC 4106401 |
| ල - 1 ේ |
| 235 rIleThrileHisPheIleProAspAlaAsnThrAlaAlaLysLeuPheA 252 ::: ::::: 4106350TTTGCGATTCGAGTTCTACGCCAATCTGGACACCGCCTATGCCGACTTGC 4106301 |
| 252 snglnglyLysLeuAsnTrp&lnglyProProTrpGlyGluArg 266 ::: ::: ::: |
| euHisSe 2 |

| | <pre>seq_documentation_block: Sequence 20, Application US/09385028 Patent No. 632106 GENERAL INFORMATION: APPLICANT: Susan E. Jensen</pre> |
|----------------|--|
| | seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-385-028-20 |
| | 515 nLeuGlyValSerProThrGlyValValAspPhe 526 ::: ::: ::: ::: 4105510CGTCACCGTCACCTGGAATGGTCTGCCCGACTAC 4105477 |
| 515 4105511 | 499 ProIleTyrHisAspAlaPheGlnPheAlaMetAsnLysLysLeuSerAs: |
| 498 4105561 | |
| 484 4105605 | erGluLeuV ACGAGCTGG |
| 467 4105655 | 451 ProSerGlyValProProTyrAlaIleAsnHisLysAspPheLeuGluIl . ::: ::: 4105704GGCGCCGGATCCAACGACGTCGGCTACATCAACCCCGGAATTCGACGCGGC |
| 450 4105705 | 435 heAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAlaTyr |
| 435 4105755 | |
| 418 4105777 | |
| 401 4105822 | 386 erSerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrpLys :: ::::::: :::::: 4105871ACAGCATCAAGAACGTGTTGGGCATCGATGGGGCGGCGCGCGC |
| 386 4105872 | 369 nIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePheProValSers |
| 369 4105921 | 353 ArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGluGluLeuGl ::: ::: ::: 4105959GCCGATGCGATCTCACCGTGGAGCGGGCCGGTACGCGGATC |
| 352 4105960 | 338 snIleHisSerTyrProGluHisGlnLysGlnGluMetAlaGln |
| 338 4106010 | 332AspHisLeuLeuProThrA |
| 331 4106060 | 316 LysGluAlaLeuValSerThrIlePheLeuGlyArgAlaLysThrAla:::::::::::::::::::::::::::::::::: |
| 315 410611 | 300 roLeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAsp :::::: :: ::: :::::: :::::: |
| 300 410616 | 283 rPheAspValAlaGlyThrSerTrpLeuThrPheAsnIleAsnLysPheP :::::: |
| 410620 | 4106250GTCTACCAGCGCGACCTGGGCGACCACGCTACCAGCGGGCCCGCAGCGAT |

| = LysLeuLysSerAlabheTrpSerAsnGlyAspProLeu |
|--|
| ω σ |
| 67 lyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGlu 79 |
| 50 gGlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluG 67 :::::: |
| 34 GlyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProAr 50 |
| Align seg 1/1 to: US-09-385-028-20 from: 1 to: 1668 |
| alignment_block: US-09-824-567-2 x US-09-385-028-20 |
| alignment_scores: Quality: 165.50 Length: 462 Ratio: 0.710 Gaps: 17 Percent Similarity: 50.433 Percent Identity: 20.996 |
| ADDRESSED JACOSSON, PRICE, HOLMAN & STERN, PPLC STREET: The Jenifer Bullding, 400 Seventh Street, N.W. CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM FC COMPAULISH COMPUTER: IBM FC COMPAULISH COMPUTER: PAPPLICATION SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION NUMBER: US/09/385,028 FILING DATE: APPLICATION NUMBER: US/09/385,028 FILING DATE: 29-JAN-1997 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION NUMBER: US/09/385,028 FELEPHONE: D. DOUGHAS PRICE REGISTRATION NUMBER: US/09/385,028 FELEPHONE: Q20 538-6666 TELEPHONE: (202 638-6666 TELEPHONE: C202 39305350) INFORMATION FOR ESQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1668 base pairs FUNDECULE TYPE: DNA (genomic) US-09-385-028-20 |
| TITLE OF INVENTION: NUMBER OF SEQUENCES: |
| שי |

| 5 | erSerLeuLeuValGlnLeuTleArgGlnGln 3 | |
|------------|--|--|
| 83 153 | 300 GGIULEUGINILEThrAlaLysAspLeuGluHisLeuAsnLeuIlePheP 30 | |
| 103 | 50 MetAlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGl 3 | |
| .083 | 33 isLeuLeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGlu 3 | |
| 033 | 19 uValSerThrIlePheLeuGlyArgAlaLysThrAlaAsp | |
| 319 989 | etLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLe 3 :: ::: ::: ::: ::: ::: TGCACTGCCGGGGGCCGTGCAGTTCGCCACCGACAAAGCGGCCAT 9 | |
| 302 | 287 laGlyThrSerTrpLeuThrPheAsnIleAsnLysPheProLeuAsn 3 :: ::: ::: | |
| 287 389 | 270 uThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerPheAspValA 2 | |
| 270 846 | 0 GlyProProTrpGly | |
| 259 804 | spAlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGln ::: | |
| 243 754 | ValGluThrLysThrIleThrIleHisPheIleProA ::::::::: ::: ::: TGCGCGTCCAGCGCCTCCCGGATCGAGGTGCACCTCGGCAAGG | |
| 23C | LysGlnTrpIleLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGl ::: | |
| 213 654 | ysSerLeuProIleAlaSerGlyAlaPheTyrFroLysAsnIleLysGln :: ::: ::: GGCTGCGGCCCGTGGCGACCGGCCCGTACCGGATCGTCTCGTACACCCGG | |
| 197 | 181 uProValPhePheProValHisLysSerGlnArgThrLeuGlnSerL | |
| 18: | 165 ValValThrLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLe | |
| 50 | 6ValHis 5 CGGACGCCGACGGACCGGTGACGCTGGAG | |
| 4 F 5 5 | 144 eGlnGluGlyHisLeuSerIleAspHisPheGly | |
| 14 | SASnValA | |
| 12 37 | 11 hralaGluAspPheIleGluSerTrpLysGlr :::: ::: ::: 35 TCTCGGCCGACATCAAGCA | |

| Ouality: 165.50 Length: 462 Ratio: 0.710 Gaps: 17 Percent Similarity: 50.433 Percent Identity: 20.996 | TELEX: RCA 24893 III INFORMATION FOR SEQ ID NC SEQUENCE CHARACTERISTIC LENGTH: 11604 base p TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (ge | PRIOR APP PRIOR APPLICA ETLING ETLING ATTORNEY NAME: REGISTR REFEREN TELECOMMU TELEPHO TELEPHO | COUNTRY: U.S.A. 2 IP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/385,028 FILING DATE: CLASGIFFORTOM: | NUMBER CORRESE ADDRE STREE CITY: | Patent No. 6232106 Patent No. 6232106 GEMERAL INFORMATION: APPLICANT: Susan E. Jense APPLICANT: Kwamena A Aidd APPLICANT: Ashish S. Parer TITLE OF INVENTION: DNA SPATENT NO. 6232106 | | . H:e | _ | 400 TrpLysGluSerLeuGlyPheAlaIleProIleValGlyLysGluPheAl 416 | 1154 GCTTCCGCACCAGGATCGCCGCCAGGACCGGCTCAAGGACTACCGG 1203 |
|---|---|--|--|----------------------------------|---|--|-------|---|--|--|
|---|---|--|--|----------------------------------|---|--|-------|---|--|--|

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alignment_block:
US-09-824-567-2 x US-09-385-028-13
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8055 ....CTCGCCGAGCCGGAGCTGCGCGCGCGCGCGCACAC...CCGCTGA 8097
                                                                                                                   8013 CTCGCGGGCTTCGGTGTGCAGCCCGCGGCCCAGGAGCGCATC..... 8054
                                                                                                                                                                                                                                            7963 ACCCGCACGAGGTGGACCGCATGCTGCTGGCGGGGGGAGGCCCATGTGGAC 8012
                                                                                                                                                                                                                                                                                                                                                                   7913 CCCGGTGCGCGTCCAGCGCGCCTCCCCGGATCGAGGTGCACCTCGGCAAGG 7962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7863 GGCGAGCTGGCCGTCCTGGAGCCCAATCCGCACTGGGACCCCGAGACCGA 7912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7813 GGCTGCGGCCGTGGCCACCGGCCCGTACCGGATCGTCCTCGTACACCCGG 7862
                                                         270 uThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerPheAspValA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7763 GCCGTCCACCACCCCGTGCCGCGCGACCGGGACACCGGCGCGCGAGTACC 7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7713 GTCTTCCGGCTGCGGGAGCCGTTCGCGGGGATGGATCTGCTGGCGACCAT 7762
                                                                                                                                                                         260 GlyProProTrpGly.......GluArgIleProGlnGl 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7663 CGGACGCCGACGGACCGGTGACGCTGGAGACCCCGGACGACGCTG
                                                                                                                                                                                                                                                                                                      243 spalaasnThrAlaalaLysLeuPheAsnGlnGlyLysLeuAsnTrpGln 259
                                                                                                                                                                                                                                                                                                                                                                                                                            230 n...........ValGluThrLysThrIleThrIleHisPheIleProA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 ysSerLeuProIleAlaSerGlyAlaPheTyrProLysAsnIleLysGln 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 uProValPhePheProValHisLysSerGlnArgThr...LeuGlnSerL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7613 CTACTTCCGCCACCTCCTGGGCACCGAGTACGGCGGCCCCCTGGCGGGAGC 7662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7581 TACGGCACCGATGTCCTGGGCGCCGGTCCG.....AC 7612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7543 TCTCGGCCGACATC.....AAGCACGCCATCGCCCGCAGCAAC 7580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7493 GACCTACCGGCTGCGCGAGGGCCTGCGCTACGAGGACGGCACGCCGGTCG 7542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7443 CCCGACCTCGCCGAGTCGCTGGGGGGAGTCCTCCGAGGACGGCCGGGTCTG 7492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 ValValThrLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLe 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7393 CGCTGGTCACCTTCGACACCGCGCGCGGCAAGGCGGCCAGCGGCTCGTG 7442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7343 CAACACGTACTACGCCTACACCTGGAACTTCCTCCGGCTCATCGGCCGGA 7392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 eGlnGluGlyHisLeuSerIleAspHisPheGly.................. 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 SerGlyIleTyrAlaPheAlaLeuAsnProlleLysAsnValArgLysIl 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 hrAlaGluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluVal 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 rThrPheLysLeuLysSerAlaPhe...TrpSerAsnGlyAspProLeuT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 ProAlaLeuAlaGluAspTyrSerLeuSerSer...AspGlyLeuThrTy 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 lyLeuValGlnGluAsnAsnLeuSerGly.....AsnIleGlu 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 gGlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GlyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProAr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....ValHisSerProAsnGluSerThrLeu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7712
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-385-028-1
                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
MEDIUM TYPE: FLOORY
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION DATA:
APPLICATION UMBER: US/09/385,028
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8556 TGGGGCGCCGACTTCCCCGACGGATACGGCTTCCTC 8591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8506 GCTGCCCGGAGTATCTGCGCGAGCACGGGATCGGGATCATCATGTTCGGC 8555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8462 GGTGCTG.....GACTTCCCGTCGGGCGACTACTTCGACCGCTACGGCG 8505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8412 GCCGCCGAGGCGCTGGCCGGGGCTCGCCCGGGTCGGCATCGAGGCCGGA 8461
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 TrpPheAlaAspPheAlaAspProMetAlaPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8312 CGACCTGGAGGCCGCCCCGCGCGAGCTGAAGCTGGCCGGGATGCCCGACG 8361
                                                                                                                                                                                                                                    STREET: The Jenif
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 .....SerLeuAlaThrGlyGly 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8292 GTCGGC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8242 CCCTGCTGCCCCCGACCCTCGACGGCTACAAGCACTTCGACCGGCTACCCG 8291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8198 GCAGGAGGCG.....TACGGCGGCGCGGTGGGCGGCGACATCGCGACCA 8241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 TrpLysGluSerLeuGlyPheAlaIleProIleValGlyLysGluPheAl 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8148 AATGTGCACTGCCGGCGGCGGCGTGCAGTTCGCCACCGACAAAGCGGCCAT 8197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8098 CCGCCTTCACCTGGATCTACTGCCTGTCGAGCCGGATCGCCCCGTTCGAC 8147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 roValSerSerAlaSerSerLeuLeuValGlnLeuIleArgGluGln 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 uGluLeuGlnIleThrAlaLysAspLeuGluHisLeuAsnLeuIlePhep 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 MetAlaGlnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGl 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 isLeuLeuProThrAsnIleHisSerTyrProGluHisGlnLysGlnGlu 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 laGlyThrSerTrpLeuThrPheAsnIleAsnLysPhe...ProLeuAsn 302
                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aLeuLeuGlnAlaAspLeuSerSerGlyAsnPhe......427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTCCGCACCAGGATCGCCGCCGCAAGGACCGGCTCAAGGAGTACCGG 8411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLe 319
                                                                                                                                                                                                                                                                    E: JACOBSON, PRICE, HOLMAN & STERN, PPLC
The Jenifer Buliding, 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                        Acid Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequence Encoding Enzymes of Clavulanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....CCCGAGGGCACCGG 8311
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alignment_block:
US-09-824-567-2 x US-09-385-028-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces clavuligerus US-09-385-028-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-385-028-1 from: 1 to: 15079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                             9695 CGGACGCCGACGGACCGGTGACGCTGGAGACCCCGGACGACGCGTG
                                                                                                                                           9645 CTACTICCGCCACCTCCTGGGCACCGAGTACGGCGGCCCCTGGCGGGAGC 9694
                                                                                                                                                                                                                            9613 TACGCCACCGATGTCCTGGGCGCCGGTCCG......AC 9644
                                                                                                                                                                                                                                                                                                                  9575 TCTCGGCCGACATC.....
                                                                                                                                                                                                                                                                                                                                                                                                   9525 GACCTACCGGCTGCGCGAGGGCCTGCGCTACGAGGACGGCACGCCGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9475 CCCGACCTCGCCGAGTCGCTGGGCGAGTCCTCCGAGGACGGCCGGGTCTG 9524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: RCA 248593 IDEA OR INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9425 CGCTGGTCACCTTCGACACCGCGCCCGGGCAAGGCGGGCCAGCGGCTCGTG 9474
165 ValValThrLeuGluSerProThrSerHisPheLeuLysLeuLeuAlaLe 181
                                                                                                  156 ......ValHisSerProAsnGluSerThrLeu 164
                                                                                                                                                                                   144 eGlnGluGlyHisLeuSerIleAspHisPheGly.................. 155
                                                                                                                                                                                                                                                                      128 SerGlyIleTyrAlaPheAlaLeuAsnProIleLysAsnValArgLysIl 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9375 CAACACGTACTACGCCTACACCTGGAACTTCCTCCGGCTCATCGGCCGGA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 hrAlaGluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluVal 127
                                                                                                                                                                                                                                                                                                                                                                                                                                        95 rThrPheLysLeuLysSerAlaPhe...TrpSerAsnGlyAspProLeuT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 ProAlaLeuAlaGluAspTyrSerLeuSerSer ... AspGlyLeuThrTy 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 lyLeuValGlnGluAsnAsnLeuSerGly.....AsnIleGlu 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 gGlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTyrGluG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 GlyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAspProAr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: D. Douglas Price
REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 39305350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165.50
0.710
50.433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/790,462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 20.996
                                                                                                                                                                                                                                                                                                                  .AAGCACGCCATCGCCCGCAGCAAC 9612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1418/P57452US2
                                                               9744
                                                                                                                                                                                                                                                                                                                                                                                                   9574
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| | AspProMetAlaPheLeu 445 | 434 |
|--------------------|--|-------------|
| 587 | CTGCCCGGAGTATCTGCGCGAGCACGGGATCGGGATCATCATGTTCGGC 10 | 0538 |
| | SerlenalaThrClvClv /3 | 428 |
| 7 | aLeuLeuGinAlaAspLeuSerSerGlyAsnPhe | 416 0494 |
| 493 | sacacraaccacacacaccaaardaacardaadacaaa 10 | 44 |
| 6 | TrpLysGluSerLeuGlyPheAlaIleProIleValGlyLysGluPheAl 410 | 400 |
| 443 | GTACCGG 10 | 0394 |
| 9 | SerAlaSerSerLeuLeuValGlnLeuIleArgGluGln 39 | 383 |
| 393 | UsinLeuGinileThrAlaLysAspLeuGluHisLeuAsnLeuIlePheP 38::: ::::::::::::::::::::::::::::::: | 0344 |
| 343 | TCGGCcccgAgggcAccgg 10 | 0324 |
| o | lnArgGlnAlaTyrAlaLysLysLeuPheLysGluAlaLeuGl 36 | w |
| 323 | CCCTCGACGGCTACAAGCACTTCGACCGCTACCCG 10 | 0274 |
| 9 | sSerTyrProGluHisGlnLysGlnGlu 34 | 333 |
| 1273 | HIT THE STATE OF T | 0230 |
| u | alSerThrIlePheLeuGlyArqAlaLysThrAlaAsp н ३३ | 319 |
| .9 | AsnMetLysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLe 31 ::: | 303 0180 |
|)2)179 | laGlyThrSerTrpLeuThrPheAsnIleAsnLysPheProLeuAsn 30 ::: ::: :::: | 287 |
| 17)129 | uThrLeuSerAsnLeuGlnSerLysGlyHisLeuHisSerPheAspValA 28 | .0087 |
| 0086 | GlyProProTrpGlyGluArgIleProGlnG1 27 :::: cTCGCGGGGCTTCGGTGTGCAGCCCGCGGCCCAGGAGCGCATC 10 | 260 |
|))) (44 | SpAlaAsnThrAlaAlaLysLeupheAsnGlnGlyLysLeuAsnTrpGln 25 | 243 9995 |
| 13 | nValGluThrLys' : : : : : : : : : : : : : : : : : : : | 230 9945 |
| 30 | LysGlnTrpIleLysLeuSerLysAsnProHisTyrTyrAsnGlnSerGl 23 | 214 9895 |
| 13 | 7 ysSerLeuProIleAlaSerGlyAlaPheTyrProLysAsnIleLysGln 21 :: ::: ::: 5 GGCTGCGGCCCGTGGCGACCGGCCCGTACCGGATCGTCTCGTACACCCGG 98 | 197 9845 |
| 97 844 | uProValPhePheProValHisLysSerGlnArgThrLeuGlnSerL 19 | 181 9795 |
| 794 | GTCTTCCGGCTGCGGGAGCCGTTCGCGGGGAT | · . |

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alignment_block:
US-09-824-567-2 x PCT-US96-05320A-113
                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: double;
TOPOLOGY: linear
PCT-US96-05320A-113
                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 113, Application PC/TUS9605320A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: June 7, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429

FILING DATE: June 7, 1995

APPLICATION NUMBER: 08/487,429

FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Eric K. Steffe

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.014

TELECOMMUNICATION INFORMATION:

TELEPAN: (202) 371-2600

TELEPAN: (202) 371-2600

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 backs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US96-05320A-113
                                                                                                                             Align seg 1/1 to: PCT-US96-05320A-113
                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
ZIP: 2003-3934
ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
    22 yCysLys....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: J. Craig Venter
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome
NUMBER OF SEQUENCES: 48
                                                                            6 ValGlyIleCysIleThrIleLeuLeuSerLeuSerValValLeuGlnGl 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                       1 ATGAATATTTTAATTAATAAACGTATCTTTTTATTAGTTACCCCTTGTAGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2232 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: A CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                Quality:
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Rockville, MD 20850
United States of America
Johns Hopkins University
720 Rutland Avenue
Baltimore, MD 21205
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mark D. Adams
Owen White
Hamilton O. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Genome Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IUMBER: PCT/US96/05320A
April22, 1996
                                                                                                                                                                                                                                  138.50
0.478
44.343
.GluSerSerHisSerSerThrSerArgG 34
                                                                                                                                                                                                                              Length: 654
Gaps: 32
Percent Identity: 18.807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1488.014PC01
                                                                                                                           from: 1
                                                                                                                           to: 2232
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| 01 | 255 | eHisPheIleProAspAlaAsnThrAlaAlaLysLeuPheAsnGlnGlyL::::::: ::: | 238 |
|---------------|------------|--|------------|
| or as | 238 905 | GluThrLysThrIleThrI ::: AAAATTACACATTAAAAT | 222 856 |
| 5, 1 | 221 855 | Prolysasnīlelysglnlys ::: AIGCGTTATGGTACTGATATA | 1 0 |
| 7 6 | 205 817 | rGlnArgThrLeuGlnSerLysSerLeuProIleAlaSerGlyA: ::: ::: ::: ; : | 190 768 |
| 0 | 19 76 | GAG | 178 718 |
| 7 | 177 717 | alThrLeuGluSerProThrSerHisPheLeuLys | 166 |
| 7 6 | 66. | rThr CAAA | 150 618 |
| 0 | 15 | AsnProIleLysAsnValArgLysIleGlnGluGlyHisLeuSe | 136 574 |
| ωσ | 13 57 | raataatagcaataataaccaaa | 131 524 |
| 3 0 | 13 52 | rpLysGlnValAlar : | 116 489 |
| σο σ <i>ι</i> | 48 | AspProLeu ::: GAACAGTAAAATTTGAAACTAAG | 108 439 |
| 8 7 | 10 | bysSeralaph | |
| ω | 38 | UATACCAACAGGGTTCTATTTTTTTTGAGCCTGAATTD | 96 339 |
| ω | 33 33 | aGluAspTyrSerLeuSerSerAspGlyL GAAGATGTTAGAGTGCAGTTAGATGGGG | |
| 00 | 28 | AsmIleGluPro | 73 239 |
| ∞ | 73 | HisIleTyrGluGlyLeuValGlnGl ::: AGCAAATTTAATTAATATCTTGCCAGGTGTG | 63 201 |
| 0 | 62 20 | roargGlnValargLeuLeuSerGluIleSerLeu ::: CGTTCAGTATTAAAACAGAAAATATCGAACAA | 48 151 |
| 0 | 47 15 | CCTATTAT | 34 101 |
| 0 | 10 | TATTCAACTAAATGTAACCGCAAAACNAAATTCTTCTAATTCTAATAGAG | 51 |

| | 906 | CAACTATCTACCTGAAAATAACCCATGGATTAACTTATCTACTCAG 9 | 951 |
|----------|-------|---|------|
| | 255 | | 271 |
| | 952 | ACAAAATGATATGCGTCCCAAAGAAGCA | 999 |
| | 272 | LeuSerAsnLeuGlnSerLysGlyHisLeuHisSerPheAspValAlaGl 2 | 88 |
| — | .000 | AGCTTAGGTAA 1 | 028 |
| | 288 | ŤL 3 | 05 |
| ₽-I | 029 | : : 1 | 074 |
| | 305 | ysLeuArgGluAlaLeuAlaSerAlaLeuAspLysGluAlaLeuValSer 3 | 21 |
| ь | 1075 | | 1107 |
| | 322 | | 26 |
| Д | 108 | TTGCAATGGTTAAAAAACACAAGAAATACTTTAAT | 1157 |
| | 327 | ArgAlaLysThrAlaAspHisLeuLeuProThrAsnI 3 | 39 |
| щ. | 158 | : | 188 |
| | · · | eHisSerTyrProGluHisGlnLysGlnGluMetAlaGlnArgGlnAla 3 | U |
| j | F.B.T | ATAATTATGGCTATTCCAACCCTATTATATGCCATCTGGACGTCAA I | 236 |
| | G | luLeuGlnIleThrAl 3 | 72 |
| سو | 237 | ATACACAGGCGTTTTATTTACAA | 260 |
| | 372 | erSerAlaS 3 | œ |
| j | 261 | : : : : : | 299 |
| | 389 | erSerLeuLeuValGlnLeuIleArgGluGlnTrpLysGluSerLeuGly 4 | 05 |
| | 1300 | | 329 |
| | 406 | PheAlaIleProIleValGlyLysGluPheAlaLeuLeuGlnAlaAspLe 4 | 22 |
| | 1330 | - | 361 |
| | 422 | rGlyAsnPheSerLeuAlaThrGlyG 4 | 33 |
| <u></u> | 362 | CAGGACATGATTATAGCCAGAAAAATTATAAT | 399 |
| | 433 | lyTrpPheAlaAspPheAlaAspProMetAlaPheLeuThrIlePheAla 4 | 49 |
| ш | 1400 | TCT 1 | 407 |
| ٠ | 450 | roProTyrAlaIleAsnHisLysAspPheLeuGl 4 | 66 |
| , | | | 4 |
| | 466 | ulleLeuGlnAsnlleGluglng 47 | 74 |
| | 7 | | > 1 |
| _ | 474 | LUGINASPHISGINLYSATGSerGluLeuValSerGlnAlaSerLeuTyr 4 :::::::::::::::::::::::::::::::::::: | 546 |
| | 491 | Th 4 | 93 |
| щ | 549 | TAATCAAACGAGAGTGGGTGGAATTATTACTCT 1 | 598 |
| | 493 | rPheHisIleIleGluProIleTyrHisAspAlaPheGlnPhe 5 | 07 |
| ш | 599 | AATGATGCTTTTCAATTTAGAACTA 1 | 642 |

| 508AlaMetAsnLysLysLeuSerAsnLeuGlyVal 518 ::: ::: ::::::: 1643 CTTATTTTACAATCGCGGCAAGAATGAAATATTTAAAACCAGAGGACTT 1692 |
|--|
| 519 SerProThrGly 522 ::: ::: 1693 AATTGTGTAGGC 1704 |
| eq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-462-467B-3 |
| IS/084 |
| APPLICANT: Rosenbaum, Jan S TITLE OF INVENTION: The Use of a BMP Protein Receptor TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I TITLE OF INVENTION: BMP Receptor NUMBER OF SEQUENCES: 39 NUMBER OF SEQUENCES: 39 |
| ADDRESSEE: The Procter & Gamble Company STREET: 11810 East Miami River Road CITY: Ross STATE: OH |
| |
| otIn Release # ON DATA: BER: US/08/46 |
| CLASSIFICATION: CLASSIFICATION: TTORNEY/AGENT INE NAME: Hersko, E REGISTRATION NUM REFERENCE/DOCKET |
| TELEPHONE: (513) 627-0633 TELEPHONE: (513) 627-0633 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2156 base pairs TYPE: nucleic acid |
| - # ` |
| lignment_scores: Quality: 117.00 Ratio: 0.544 Percent Similarity: 44.330 Percent Identity: 21.031 |
| lignment_block: US-09-824-567-2 x US-08-462-467B-3/rev |
| Align seg 1/1 to reverse of: US-08-462-467B-3 from: 1 to: 2156 |
| 4 IleSerValGlyIleCysIleThrIleLeuLeuSe 15 ::: |
| 15 rLeuSerValValLeuGlnGlyCysLysGluSerSerHisSerSerThrS 32 :::::: ::::::::::::::::::::::::::: |
| 32 erargGlyGluLeualaIleAsnIleArgAspGluProArgSerLeuAsp 48 |

| 296 | 89 hrSerTrpLeuThrPheAsnIle | 22 |
|-------------|---|-----------|
| 1154 | 03 CTCATCTCCAACTATAAAGCGGGCAATGTTGTCATGTTCCATCAAAGGCA | 120 |
| 289 | 3 erAsnLeuGlnSerLysGlyHisLeuHisSerPheAspValAlaGlyT | 27 |
| 273 1204 | 9 nGlyProProTrpGlyGluArgIleProGlnGluThrLeuS :::: ::: 3 TAGTACTCCATCACAAGCAAATATTCCATGCGTCCATCTGCAGTGACTCT | 25 125 |
| 259 1254 | 3 ASPAlaASnThrAlaAlaLySLeuPheAsnGlnGlyLySLeuAsnTrpGl ::::: :: GACTTAAATACTTGCATAAAGATCCATTGGGA | 24 128 |
| 242 1286 | 35 AGTAACAGAATGAGCAAGAGCGCAAGAGCTTACCCAGTCACTTGTGTGGA : | 13 |
| w Ki | 23 TIYESS. | . 13 |
| 225 1385 | 09 LysAsnIleLysGlnLysGlnTrpIleLysLeuSerLysAsnProHisTy | 14 2 |
| 208 1412 | 03 er | 14 |
| 203 1462 | OVALHISLYSSerGlnArgThrLeuGlnSerLysSerLeuProIleAlas | 14 1 |
| 186 1487 | 3 | 15 |
| 171 1535 | 62 erThrLeuValValThrLeuGluSerPro | H 5 H |
| 162 1585 | .45 nGluGlyHisLeuSerIleAspHisPheGlyValHisSerProAsnGluS | 16 |
| 145 1635 | 129 GlyIleTyrAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGl | 16 |
| 128 1676 | 12 1aGluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValSer | 1 17 |
| 112 1717 | 99 LeuLysSer.AlaPheTrpSerAsnGlyAspProLeuThrA :::::: ::::: :::::: | 17 |
| 98 1767 | 82 euAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLys | 17 |
| 82 1788 | 65 rGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaL ::: | 18 |
| 1809 | ::: 32 GACCTCACTGCCAGGCTA | 18 |
| 65 | ArgLeuLe | |
| 1833 | | 18 |

Gaps: 24
Percent Identity: 21.031 Length:

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-334-179A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08334179A Patent No. 6306622
                                                                                                                                TELEFAX: 513-627-0260 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1003 CAAGAGAGGGTTCGGATGCTGCCTCCATCATGTTCATACTGTGAAGA 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1053 TCCATATCGACCTCGGCCAATCAGCTCCAACAGTTTCAGATTATCTAGAT 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1103 AACACTTTTACAGCAACTGGACGCTCATCCAAGGAGCCTTTATATACTGC 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1153 CTCTGTAAATGTTCTTTTCGTTGATAAAATTCTGACGGTTTGCAAAGGAA 1104
                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2157 base pairs
                                                                                                                                                                                       REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-627-2858
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORSTANJE, BRAHM J.
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            856 TCTCATCTCGGTTAAATGAATGAGGTGGACTGAGTGGTGTTGTGTCAGGA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 alSerSerSerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrp 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  806 GGTGGAAAATTCTCAGTAAAGTTGACATTACATAAATCTGTGCTAC.... 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 ......ProThrAsnIleHisSerTyrProGluHisGln. 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 heLysGluAlaLeuGluGlu.....LeuGln.IleThrAlaLysAs 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         906 AACTATCAAAACAGCTAATACAGAGACTGATGCCAAAGCAATGATTATTG 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   953 CCTTGTTTACGGTCTCCTGTCAACATT...CTGTATCCAAAGCATAAGGC 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 aLeuAspLysGluAlaLeuValSer.....ThrIlePheLeuGlyArgA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 AsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAl 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
TOPOLOGY: linear
                               STRANDEDNESS:
                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......LysGlnGluMetAlaGlnArgGlnAlaTyrAlaLysLysLeuP 361
                         nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            НО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11810 EAST MIAMI RIVER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROSENBAUM, JAN S.
NOHNO, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                        US/08/334,179A
                                                                                                                                                                                                                                             5473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-824-567-2 x US-08-334-179A-3/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-334-179A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 0.544
Percent Similarity: 44.330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: US-08-334-179A-3 from: 1 to: 2157
  1461 GTCACTAATAACACAGGTTCCATCATTTTTCACTAGGACATTTCTGCTGT 1412
                                                                                                                                                                                                                                                                                                                                   1584 CACAGCTCCTTCTAGCACTTCTGGTGCCATATATCTGATAGTGCCAACCT 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                1634 AGAGCATACATGTCTACTTGTTTCAAAGCTGATTCACAGTCCCTCAAGTT 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1675 GGTCTGTACATCTCATAAATATCTCCC.....AATAGATTAGTCCA 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1716 AAAAG......CCATCTGGTACTCTGGTACGGATTCCCCTGGGAAGA 1676
                                                                                                                                                                                                                         1534 CGCTTATGGCTGCATTATCTTCCTCCCCTGGGCGCACCAGTCTATTTC.. 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1832 GACCTCACTGCCAGGCTATTTTCT.....1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1787 .....CGTCTCTGTTTTCCCTAGAC 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1808 ...... 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1882 GCCGAGCCTCTGCATCCTGGTCCCAACAGTCTTCGATTGTCTCCTTGAGT 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1932 CCAAATCATCATAAGTTCAGCCATCCTTTCCTCAGCACACTGTGCAGTAA 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 oValHisLysSerGlnArgThrLeuGlnSerLysSerLeuProIleAlaS 203
                                                      129 GlyIleTyrAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGl 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 laGluAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValSer 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 LeuLysSer.AlaPhe......TrpSerAsnGlyAspProLeuThrA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 euAlaGluAspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheLys 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 rGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 ProArgGlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 erArgGlyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAsp 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 rLeuSerValValLeuGlnGlyCysLysGluSerSerHisSerSerThrS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 IleSerValGlyIleCysIleThrIle.....LeuLeuSe 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nGluGlyHisLeuSerIleAspHisPheGlyValHisSerProAsnGluS 162
                                                                                                                                                                                                                                                                          .....ThrSerHisPheLeuLysLeuLeuAlaLeuProValPhePhePr 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                               .....CAGTCAGCCTCATGGACAGTCCAAA 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(409..2154)
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APPLICANT:

COUNTRY: STATE: STREET:

| | ADDRESSEE: 7 STREET: 1181 |
|-------------|--|
| ~ | APPLICANT: NOSENBAUM, JAN S. APPLICANT: NOHNO, TSUTOMU TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: |
| | <pre>seg_documentation_block: Sequence 1, Application US/08334179A Patent No. 6306622 GENERAL TREPORTION:</pre> |
| | <pre>seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-334-179A-1</pre> |
| 16 | 384 alSerSerSerAlaSerSerLeuLeuValGlnLeuIleArgGluGlnTrp 40 ::: ::::::::::::::::::::::::::::::: |
| 61 4 | 06 GGTGGAAAATTCTCAGTAAAGTTGACATTACATAAATCTGTGCTAC 7 |
| ;74 107 | helysGluAlaLeuGluGluLeuGln.IleThrAlaLysAs 3 |
| ·61 ·57 | 47LysGlnGluMetAlaGlnArgGlnAlaTyrAlaLysLysLeup 3 11 |
| 46 07 | φ ω |
| 35 54 | TCATGTTCATACTGTGAAGA 9 |
| 328 1004 | 13 aLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyArgA |
| .13 .054 | 297 AsnlysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaSerAl 3 |
| .104 | 89 hrSerTrpLeuThrPheAsnIle |
| 289 1154 | isLeuHisSerPheAspValAlaGlyT ::: ::::: CAATGTTGTCATGTTCCATCAAAGGCA |
| 73 | 259 nGlyProProTrpGlyGluArgIleProGlnGluThrLeuS 27 :::: ::: 1253 TAGTACTCCATCACAAGCAAATATTCCATGGGTCCATCTGCAGTGACTCT 12 |
| 259 254 | 243 AspAlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTrpGl 2 |
| .286 | 228GlnSerGlnValGluThrLysThrIleThrIleHisPheIlePro 2 :::::::::::::::::::::::::::::::::: |
| 227 | |
| 225 1385 | 209 LysAsnIleLysGlnLysGlnTrpIleLysLeuSerLysAsnProHisTy 2 ::: 1411 TTAAATCTCGATGGGAAATTGCAGGTT |

| 99 Leulysser.AlaPheTrpSerAsnGlyAspProLeuThrA | 2 euAlaGluAspTy 77 | 65 rGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnIleGluProAlaL::: ::: 1808TTCCAGGCTTCTGGGAACTTG | 49 ProArgGlnValArgLeuLeuSerGluIleSerLeuValLysHisIleTy ::: ::: 1832 GACCTCACTGCCAGGCTATTTTCT | 32 erArgGlyGluLeuAlaIleAsnIleArgAspGluProArgSerLeuAsp :::::::::::::::::::::::::::::::: | 15 rLeuSerValValLeuGlnGlyCysLysGluSerSerHisSerSerThrS | 4 IleSerValGlyIleCysIleThrIle | Align seg 1/1 to reverse of: US-08-334-179A-1 from: 1 to | alignment_block: US-09-824-567-2 x US-08-334-179A-1/rev | alignment_scores: Quality: 117.00 Length: 485 Quality: 0.544 Gaps: 24 Percent Similarity: 44.330 Percent Identity: 21.031 | CITY: ROSS COUNTRY: US ZIP: 45061 COUNTRY: US COUNTRY: US COMPUTER FRADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.30, Version #1.30 CURRENT APPLICATION NUMBER: US-08/334,179A FILING DATE: 04 NOV-1994 CILASSIFICATION UMBER: US-08/334,179A FILING DATE: 04 NOV-1994 CILASSIFICATION NUMBER: 5473 TELECOMMUNICATION NUMBER: 5473 TELECOMMUNICATION NUMBER: 5473 TELECOMMUNICATION INFORMATION: TELEPHONE: 513-627-0260 INFORMATION POR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3601 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE: TPE: CDNA FEATURE: TPE: CDNA FEATURE: TPE: CDNA CLCATION: join(4093522) US-08-334-179A-1 |
|--|--------------------|---|---|--|---|-------------------------------|--|--|---|--|
| 112 1717 128 | 98 1767 | 82 1788 | 65 1809 | 48 1833 | 32 1883 | 15 1933 | o: 360 | | | |

AAAAG..

.....CCATCTGGTACTCTGGTACGGATTCCCCTGGGAAGA 1676

| | P 361 G 857 | 34/LysGlnGluMetAlaGlnArgGlnAlaTyrAlaLysLysLeu |
|-----------|--------------------------|--|
| | . 346 C 907 | 36ProThrAsnIleHisSerTyrProGluHisGln. :: :: ::53 CCTTGTTTACGGTCTCCTGTCAACATTCTGTATCCAAAGCATAAGG |
| | . 335 A 954 | '28 laLysThrAlaAspHisLeuLeu |
| A. | gA 328 : AT 100 | 13 aLeuAspLysGluAlaLeuValSerThrIlePheLeuGlyAi |
| ¥. ~ | Al 313 | 97 AsnLysPheProLeuAsnAsnMetLysLeuArgGluAlaLeuAlaSes |
|)4 | 296 AA 110 | 289 hrSerTrpLeuThrPheAsnIle |
| 5, 6 | 28 11 | 0 |
| 3 | S 27 | 259 nGlyProProTrpGlyGluArgIleProGlnGluThrLeuS :::: |
| 9 | pG1 25 :: GGA 12 | 43 AspAlaAsnThrAlaAlaLysLeuPheAsnGlnGlyLysLeuAsnTy |
| 2 86 | o 24 A 12 | 28GlnSerGlnValGluThrLysThrIleThrIleHispheIleP ::::: ::::: 35 AGTAACAGAATGAGCAAGAGCGCAAGAGCTTAGCCCAGTCACTTGTGTG |
| 7 | 22 CT 13 | 225 rTyrasn |
| & VI | Ty 22 | 209 LysAsnIleLysGlnLysGlnTrpIleLysLeuSerLysAsnProHis |
| 12 | Pro 20 | 203 er |
| 62 | las 20 AAA 14 | 86 OValHisLysSerGlnArgThrLeuGlnSerLysSerLeuProIleA |
| 36 .87 | Pr 18 | 172ThrSerHisPheLeuLysLeuLeuAlaLeuProValPhePhe ::: 1 ::: 1534 CGCTTATGGCTGCATTATCTTCCTCCCCTGGGCGCACCAGTCTATTTC |
| 71 | 17 CT 15 | 162 erThrLeuValValThrLeuGluSerPro |
| 62 585 | uS 1 :- TT 1 | 145 nGluGlyHisLeuSerIleAspHisPheGlyValHisSerProAsnGl |
| 45 | G1 1 CA 1 | 129 GlyrleTyrAlaPheAlaLeuAsnProlleLysAsnValArgLysTle ::: 1675 GGTCTGTACATCTCATAAATATCTCCCAATAGATTAGTO |

| 89 | 273 erAsnLeuGlnSerLysGlyHisLeuHisSerPheAspValAlaGlyT 2 |
|-------------|--|
| 73 204 | 39 NGLYPTOPTOTTPGLYGLUARGILEPROGlngluThrLeuS 2 :::: ::: ::: 3 TAGTACTCCATCACAAGCAAATATTCCATGCGTCCATCTGCAGTGACTCT 1 |
| 59 254 | 43 ASPALAASSThrAlaAlaLySLeuPheASSGlnGlyLySLeuASSTrpGL 2 |
| 286 | 128GlnSerGlnValGluThrLy |
| 336 | |
| w | AAATCTCGATGGGAAATTGCAGGTTvrasn. |
| 25 | 209 LysAsnIleLysGlnLysGlnTrpIleLysLeuSerLysAsnProHisTy ::: |
| 208 L412 | 203 erGlyAlaPheTyrPro 2 |
| 203 1462 | 86CAGTCAGCCTCATGGACAGTCCAAA |
| 186 1487 | 34 CGCTTATGGCTGCATTATCTTCCTCCCCTGGGCGCACCAGTCTATTTC. |
| Ċπ | ACACCTCCTTCTAGCACTTCTGGTGCCATTATATCTGATAGTGCCAACCT |
| 71 | .62 erThrLeuValValThrLeuGluSerPro |
| 162 1585 | lyValHisSerProAsnGluS ::: TGATTCACAGTCCCTCAAGTT |
| 145 1635 | 29 GlyIleTyrAlaPheAlaLeuAsnProIleLysAsnValArgLysIleGl ::: :::: 75 GGTCTGTACATCTCATAAATATCTCCCAATAGATTAGTCCA |
| 6 | 16 AAAAGCCATCTGGTACTCTGGTACGGATTCCCCTGGGAAGA |
| 28 | luAspPheIleGluSerTrpLysGlnValAlaThrGlnGluValSe |
| 112 1717 | PheT ::: TATCCTCAAAAGT |
| 1767 | 7GGTCTCTGTTTTTCCCTA |
| 98 | AspTyrSerLeuSerSerAspGlyLeuThrTyrThrPheL |
| | TTCCAGGCTTCTGGGAACTTG |
| ē | 5 rGluGlyLeuValGlnGluAsnAsnLeuSerGlyAsnI |
| 65 | leSerLeuValLysHisIle |
| 48 1833 | 12 8 |
| 1883 | CCAAATCATCATAAGTTCAGCCATCCT |

| 289 hrSetTrpLeuthrPheAsnile | 289 htserTrpLeuThrpheAsnIle |
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-567-2 x US-08-743-637B-8/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                           APPLICANT: OUELLETTE, MARPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPEC
TITLE OF INVENTION: AMPL
TITLE OF INVENTION: COMM
TITLE OF INVENTION: FROM
NUMBER OF SEQUENCES: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 650586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 8:
CENTRALION TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 erHisPheLeu 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 lHisSerProAsnGluSerThrLeuValValThrLeuGluSerProThrS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AACGCCCGCGAGATTGCCCCTCGGGCAAAAGGGACCCGAGACGTTGGGGGT 66
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
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                                    STATE: Wisconsin
                           COUNTRY:
                                                                  CITY: Milwaukee
                                                                                      STREET:
                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lnGluValSerGlyIleTyrAla...PheAlaLeuAsn...ProIleLys 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
53202-4497
                                                                           411 East Wisconsin Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klebsiella pneumoniae
                                                                                                         QUARLES & BRADY
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANVIBIOTIC RESISTANCE GENES
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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alignment_block:
US-09-824-567-2 x US-08-526-840B-8/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: US-08-526-840B-8 from: 1 to: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          115
                                                                                                                                                                                                     140 AsnValArgLysIleGlnGluGlyHisLeuSerIleAspHisPheGlyVa 156
                                                                                                                  156 lHisSerProAsnGluSerThrLeuValValThrLeuGluSerProThrS 173
                                                                                                                                                                                                                                                                                      125 lnGluValSerGlyIleTyrAla...PheAlaLeuAsn...ProIleLys 139
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ORIGINAL SOURCE:
ORGANISM: Kle
                                      173 erHisPheLeu 176
                                                                                                                                                                                                                                                                                                                                     215 GGCCATTACAGCGCAGGATATCGTCTGGAGCTGGCAACGGCTGGTCTCGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                      238 GGTCTGACC.....TGGTCTGACGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
15 CCGCCTTCCTG 5
                                                                          65 GAAAGCGCTGAACGACACCACGCTGCAGGTCACTCTGACCCAGCCGAATG
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APPLICATION NUMBER: US 08/304,732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 GlyLeuThrTyrThrPheLysLeuLysSerAlaPheTrpSerAsnGlyAs 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 11-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                               AACGCCCGCGAGATTGCCCTCGGGCAAAAGGGGACCCGAGACGTTGGGGGT 66
                                                                                                                                                                                                                                                    CGGCAACAGCCTCCCCCTACGCGAGCTACCCTGGCAATATGCATATCGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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Result
No.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
         July 26, 2002, 04:38:12 ; Search time 37.11 Seconds (without alignments) 555.074 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
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2739
1 MRKISVGICITILLSLSVVL......LSNLGVSÞTGVVDERYAKEN 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105224 seqs, 38719550 residues
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Copyright (c) 1993 - 2000 Compugen Ltd
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      DB
   HOFO_ECOLI
                                Y4WM_RHISN
YEJA_ECOLI
HXC1_HAEIN
SKI3_YEAST
ABF1_MOUSE
                                                                                                                                                                                        SAPA_ECOLI
                                                                                                                                                                                                                        SAPA_SALTY
APPA_BACSU
SAPA_HAEIN
                                                                                                                          XP55_STRLI
YC80_MYCTU
AGPA_RHIME
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P06202 salmonella
Q46863 escherichia
P71370 haemophilus
P44572 haemophilus
Q51933 streptococc
P33590 escherichia
P3950 haemophilus
P76128 escherichia
                  P17883
Q61329
P34749
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P44523
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Q11041
Q14471
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EMBL; M57689; AAA62687.1; -.
EMBL; S99110; CAB13000.1; -.
PIR; S12230; S15230.
PIR; A38447; A38447.
HSSP; P66202; 1B52.
Subtiliar; B610771; oppa.
InterPro; IPR000914; SBP_bac_5; 1.
Pfam; PF00496; SBP_bac_5; 1.

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| 1 1 1 1 1 1 | license@isb-sib.ch). | | ions as l | tute of Bioinf | | | E BACTER | ached to | REQUIRED FOR SPORULATION AND COMPETENCE. | ACIDS LO | SIN-DEPENI | THIS DROTEIN IS A COMPONENT | | and is rec | "The spook locus of Bacillus subtilis | 9858; | | | 91). | tion."; | system of | 47; PubMed=1901616; | | | | p; Bacill | ns / 1 os+ r | | oppA pre | nnotation | 01-MAR-1992 (Rel. 21, Created) | • | PRT; | | ALIGNMENTS | MUTL_CHLPN | DINCLUROME | INR1_HUMAN | | BACB BACLI | HS90_PODAN | RECG_HELPJ | ADAS CABO | VTA2_XENLA | |
| | ee | - | here are no | Bioinformatics and the EMB | | | (FIGURALITY: BELONGS TO THE BACTERIAL EXTRACELLITIAR SOLITTE-RINGING | LUCATION: Attached to the membrane by | • | UP TO FIVE AMINO ACIDS LONG WITH HIGH AFFINITY. | DENT TRANSPORT SYSTEM, I | | | oligopeptide permease locus and is required for sporul | is homologous to | | | | | | Bacillus subtilis | | | | | is group; Bacillus. | 24 | | cursor. | puace) | nduto) | | 545 AA. | | ENTS | Ż | į | i k | i | Ĥ Ē | Š | <u> </u> | Ŏ C | 'A | |
| | TS-STD | and f | restrictions | ough a | | | SOLITION | a lipic | | | | | | tion | † † D | | | | | of many | | | | | | | | | | | | | | | | Q9z794 | 25/2/0 | P17181 | P23074 | 068007 | 043109 | Q9zjal | P40292 | P18709 | |
| | .ch/announce/ | or commerc | tions on its | h a collaboration EMBL outstation - | 1 | | -BINDING | a lipid anchor | • | | IT BINDS | 9 | | and | | | | | | ۵ | A.; | | | | | | | | | | | | | | | rattus norv chlamydia p | arosopi | homo sa | simian foam | bacillus li | | helicobacte | aspergillus | xenopus lae | |

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MEDLINE=92114768; PubMed=1766370; Mathiopoulos C., Mueller J.P., Slack F.J., Bukusoglu G., Sonenshein A.L.;
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NCBI_TaxID=1423;
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Best Local
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SubtLList; BG10846; dppE.
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence of the Bacillus subtilis genome between xlyA and ykor."; submitted (NOV-1997) to the EMBL/GenBANK/DDBJ databases.
-i-FUNCTION: PART OF THE BINDING-PROTEIN-DEFENDENT TRANSPORT SYSTEM FOR DIPEPTIDES; PROBABLY RESPONSIBLE FOR THE BINDING OF DIPEPTIDES
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A Bacillus subtilis dipeptide transport system expressed during sporulation.";
                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X56678; CAA40006.1; -
EMBL; AJ002571; CAA05576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         +
                                                                                                                                                                                                                             LIPID
                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                           Peptide transport; Transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S16651; S16651.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z99110; CAB13153.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             ipoprotein; Complete proteome.
                                 12 LALGLSFALMGCTANEQAGKEGSHDKAKTSGEKVLYVNNENEPTSFDPPIG--FNNVSWQ
                                                                 12 ILLSLSVVLQGC------KESSH-SSTSRGE--LAINIRDEPRSLDPRQVRLLSEISL- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING SPORULATION, INDUCTION: NUTRIENT DEFICIENCY CONDITIONS.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WITH HIGH AFFINITY. IS EXPRESSED TO FACILITATE ADAPTATION TO NUTRIENT DEFICIENCY CONDITIONS, WHICH ALSO INDUCE SPORULATION. SUBCELULAR LOCATION: Attached to the membrane by a lipid anchor function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN FAMILY 5.
 -VKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLK-SAFWSNGDPLTAEDFIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiol. 5:1903-1913(1991)
                                                                                                       143;
                                                                                                                       Similarity
                                                                                                                                                                                           543 AA;
                                                                                                     Conservative 116;
                                                                                                                                                                                                             339
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23
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23
339
                                                                                                                                                                                           61822
                                                                                                                     17.9%;
26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               1; ALT_INIT.
ALT_INIT.
                                                                                                                     Score 489.5; DB 1
Pred. No. 4.9e-27;
                                                                                                                                                                                       DIPEPTIDE-BINDING PROTEIN DPPE.
N-ACYL DIGLYCERIDE (POTENTIAL).
T -> P (IN REF 1).
; 723A346197413356 CRC64;
                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                     Mismatches 244;
                                                                                                                                                                                                                                                                                         Signal;
                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                           Sporulation;
                                                                                                     Indels
                                                                                                                                   Length 543;
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                294 FNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQKQEMA--
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                                                            DKVKWAMVSDRNTDYQMFQSGELD-----TAYVPAELSDQLLDQDNVNIVDQAGLYFYR 302
                                                                                                          KTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLT
                                                                                                                                                        VSNPAYFPVNEKVDKDNPKWFAESDTFVGNGPFKLTEWKHDDSITMEKSDTYWDKDTVKL
                                                                                                                                                                                                    LALPVFFPVHK-----SQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVET 233
                                                                                                                                                                                                                                                    WKRMLDPKKGASSAFLGYFIEGGEAYNSGKGKKDDVKVTAKDDRTLEVTLEAPQKYFLSV
                                                                                                                                                                                                                                                                                                WKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKL
                                                                                                                                                                                                                                                                                                                                           PLNNIMEGLTRLGK-DHEPEPAMAEKWSVSKDNKTYTFTIRENAKWTNGDPVTAGDFEYA
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                   351
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RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Rasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Rasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Rasai H., Kashimoto K., Mimura S., Kitakawa M., Kitagawa M., Rasai H., Kashimoto K., Mishio Y., Motomura K., Ra Nakade S., Nakamura Y., Washimoto H., Nishio Y., Oshima T., Saito N., Ra Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Saito N., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Saito N., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Saito N., Ra Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Saito N., Ra Takemoto Y., Horiuchi T., Ra Takemoto Y., Horiuchi T., Saito N., Ra Takemoto Y., Horiuchi T., R
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This SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park J.T., Raychaudhuri D., Li H., Normark S., Mengin-Lecreulx MppA, a periplasmic binding protein essential for import of the bacterial cell wall peptide L-alanyl-gamma-D-glutamyl-mesodiaminonimelate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPPA_ECOLI P77348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97251357; PubMed-9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97426617; PubMed=9278503;
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MEDLINE=98155149; PubMed=9495761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       977348;
15-DEC-1998 (Rel. 37, Careated)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Periplasmic murein peptide-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 YIDLKWADKN 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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P28843; P76829;
01-NOV-1991 (Rel. 20, Created)
01-CT-1994 (Rel. 30, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Periplasmic oligopeptide-binding protein precursor.

OPPA_ECOLI

OPPA_ECOLI

STANDARD;

PRT;

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469 VLAQASTENTVKARNADYNAAEKILMEQAPIAPIY 503
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EcoGene: EG13776; mppA.
InterPro; IPR000914; SBP_bac_5.
Pfam: PF00496; SBP_bac_5; 1.
PROSITE: PS01040; SBP_BACTERIAL_5; 1.
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                                                                                                           407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide transport; Transport; Periplasmic; Signal; Complete proteome. SIGNAL 1 22
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SWISS-2DPAGE; P77348; COLI.
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modified and this statement is not removed. Usage by and for commer
                                                                                                                                          354
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                                                                                                                                                                                                                                                                                                                             183 NFAFFPVQKANVESGKEWTKPGNLIGNGAYVLKERVVNEKLVVVPNTHYWDNAKTVLQKV
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                                                                                                                                                                                                                                                                                                                                                                                                         123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 IYEGIVQENNISGNIEPALAEDYSISSDGLTYTFKLK-SAFWSNGDPLTAEDFIESWKQV 122
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                                                              DVKLQNQEWKTYIDSRNTGNFDVIRASWVGDYNEPSTFLTLLTSTHSGNISRFNNPAYDK
                                                                                             AIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFLTIFAYPSGVPPYAINHKDFLE 466
                                                                                                                                                             EMAQRQ--AYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGF 406
                                                                                                                                                                                              YYAFNTQKGPTADQRVRLALSMTIDRRLMTEKVLGTGEKPAWHFTPDVTAGFTPEPSPFE
                                                                                                                                                                                                                             WLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSY-PEHQK-Q
                                                                                                                                                                                                                                                                                                                                                              LPVFFPVHK----SQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETKTI
                                  ILQNIEQEQDHQKRSELVSQASLYLETFHIIEPIY 501
                                                                                                                            QMSQEELNAQAKTILSAAGYGPQKPLK----LTLLYNTSENHOKIAI-AVASMWKKNLGV
                                                                                                                                                                                                                                                             TFLPINQESAATKRYLAGDID------ITESFPKNMYQKLLKDIPGQVYTPPQLGTY 293
                                                                                                                                                                                                                                                                                             TIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSK-----GHLHSFDVAGTS
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D90772; BAA14932.1; ALT_INIT.
D90771; BAA14922.1; ALT_INIT.
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-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING

PROTEIN FAMILY 5.

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Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed properties of proteins ein the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-113(1997).

-i- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE OLIGOPEPTIDE PERMEASE, A BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM, IT PEPTIDES UP TO FIVE AMINO ACIDS LONG WITH HIGH AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kashiwagi K., Yamaguchi Y., Sakai Y., Kobayashi H., Igarashi K.; "Identification of the polyamine induced protein as a periplasmic oligopeptide binding protein."; J. Biol. Chem. 265:8387-8391(1990).
                                                                                                     STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
                                                                                                                                                             Submitted (SEP-1994)
                                                                                                                                                                           Frutiger S., Paquet N., Wilkins Hochstrasser D.F.;
                                                                                                                                                                                                     STRAIN=K12 / W3110;
Pasquali C., Sanchez
                                                                                                                                                                                                                                                            Submitted (JAN-1996) to
                                                                                                                                                                                                                                                                                           STRAIN-DR112;
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                                                                                                                                                                                                                                                                                                                                                          activities of Escherichia coli reside on
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"Pyruvate-formate-lyase-deactivase and acetyl-CoA reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa K., Kitagawa M., Makino K., Mki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
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                                                                                                                                                                                                                                                                            Igarashi K
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kins M.,
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sner J.D., Rode C.K., Mayhew G.F.,
ick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli K-12.";
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, Appel R.D
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region on the
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                                      QLIREQWKESLGFALFIVGKEFALLQADLSSGNFSLATGGWFADFADFMAFLTIFAYPSG
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QR -> HG (IN REF. 2)
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MEDLINE-21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=99349693; PubMed=10422831;
Davies T.G., Hubbard R.E., Tame J.R.H.;
"Relating structure to thermodynamics: the crystal structures and binding affinity of eight Oppa-peptide complexes.";
Protein Sci. 8:1432-1444(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tame J.R.H., Murshudov G.N., Dodson E.J., Neil T.K., Dodson G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Prôteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The crystal structures of the oligopeptide-binding protein Oppa complexed with tripeptide and tetrapeptide ligands."; Structure 3:1395-1406(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hiles I.D., Gallagher M.P., Jamieson D.J., Higgins C.F., "Molecular characterization of the oligopeptide permease of
GE MNTAHYKSPAFDSIMAETLKVTDEAQRTALYTKAEQQLDKDSAIVPVYY 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #11es I.D., Higgins C.F., "Peptide uptake by Salmonella typhimurium. The periplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96363676; PubMed-8747465;
Tame J.R.H., Dodson E.J., Murshudov G.N., Higgins C.F.,
Wilkinson A.J.;
                                                                                                                                                                                                                                                                                                                                                                 U1-JAN-1988 (Rel. 06, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Periplasmic Oligopeptide-binding protein precursor.
                                                                                                                                                                                                                                                                                                              543 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligopeptide-binding protein.";
Eur. J. Biochem. 158:561-567(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=LT2;
MEDLINE=88011222; PubMed=2821267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=86274740; PubMed=3525163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94261830; PubMed=8202710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium.";
J. Mol. Biol. 195:125-142(1987).
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                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                         OPPA_SALTY
P06202;
                                                                                                                                                                                                                                           OPPA_SALTY
                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
J. Mol. Biol. 291:393-415(1999).

-!- FUNCTION: THE PROTEIN IS A COMPONENT OF THE OLIGOPEPTIDE PERKEASE, A BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM, IT BINDS PEPTIDES UP TO FIVE AMINO ACIDS LONG WITH HIGH AFFINITY.

-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%; Score 410; DB 1; Length 543;
26.1%; Pred. No. 1.9e-21;
tive 97; Mismatches 245; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ISVGICITILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: || :| || :: |
10 IAAGI-LTALIAASAATAADVPAGVQLADKQILVRNNGSEVQSLDPHKIEGVPESNVSRD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan, PF00496; SBP_bac_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
Peptide transport; Transport; Periplasmic; Signal; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA -> TP (IN REF. 1 AND 2).
EF344E7C7991CA47 CRC64;
                                                                                                                                                                                              AE008777; AAL20664.1; ALT_INIT.
25011; QREBOA.
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61292 MW;
                                                                                                                                                                        EMBL; X04194; CAA27785.1; -
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                                                                                                                                                                                     X05491; CAA29039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tub; 10KB; 09-SEP-99.
Stydene; SG10267; oppA.
InterPro; IPROGOT:
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1854, 18-NOV-98
1851, 13-Jan-99
1851, 13-Jan-99
1864, 18-NOV-98
1874, 25-NOV-98
1893, 22-FEB-99
                                                                                                                                                                                                                                                                                                                             18-NOV-98.
18-NOV-98.
16-DEC-98.
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18-NOV-98.
                                                                                                                                                                                                                    10LA; 31-JUL-94
20LB; 29-JAN-96
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                                                                                                                                                                                                                                                              15-MAY-97
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                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-98
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1846; 13-JAN-99.
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1B52; 27-JAN-99.
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                                                                                                                                                                                                        A25011;
                                                                                                                                                                                                                                                                                                                                                             1B3G;
1B3H;
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1B4H;
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Best Local Simi
Matches 136;
                                                                                                                                                                                                                                                   lJET;
                                                                                                                                                                                                                                                                                            2RKM;
1B05;
1B0H;
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1B2H;
1B3F;
                                                                                                                                                                                                                                         10LC;
                                                                                                                                                                                                                                                                                   1RKM;
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10KB;
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64 IYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLK-SAFWSNGDPLTAEDFIESWKQV 122
                   ATQEVSGIYAFAL - - NPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLA 180
                                                                                          ---QRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETK 234
                                                                                                                                                                                                                                    246 QVIYLPISSEVTDVNRYRSGEIDMI ----YNNMPIELFQKLKKEIPNEVRVDPYLCTYYY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                         409 KKNLGVNVNLENQEWKTFLDTRHQGTFDVARAGWCADYNEPTSFLNTMLSDSSNNTAHYK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Periplasmic (Potential).
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MFDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III., Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mau B., Shao Y.;
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electrophoresis 20:2181/2195(1999).
-!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
                                                                                                                                                                                                      235 TITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNLQSK--GHLHSFDVAGTSWL
                                                                                                                                                                                                                                                                      293 TFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSY------
                                                                                                                                                                                                                                                                                                       302 EINNQKAPFNDVRVRTALKLALDRDIIVNKV----KNQGD--LPA--YSYTPPYTDGAKL
                                                                                                                                                                                                                                                                                                                                         343 --PEHQKQEMAQRQAYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQLIREQW
                                                                                                                                                                                                                                                                                                                                                                         354 VEPEWFKWSQQKRNEEAKKLLAEA----GFTADKPLTFDLLYNTSDLHKKLAI-AVASIW
                                                                                                                                                                                                                                                                                                                                                                                                         401 KESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFLTIFAYPSGVPPYAIN
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coli by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fountoulakis M., Takacs M.F., Berndt P., Langen H., "Enrichment of low abundance proteins of Escherichia hydroxyapatite chromatography.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIEPIYH 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 SPAFDKLIADTLKVADDTQRSELYAKAEQQLDKDSAIVPVYY 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative binding protein ygiS precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 AA.
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IDENTIFICATION BY MASS SPECTROMETRY.
MEDLINE=99420866; Pubmed=10493123
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15-JUL-1999 (Rel. 38, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN FAMILY 5.
                                                                                                                                        LPVFFPVHKS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 LKSAF-WSNGDPLTAEDFIESWKQVATQEVSGIYA--FALNPIKNVRKIQEGHLSIDHFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                               97 LRSGLQWSDGQPLTAEDFVLGWQRAVDPKTASPFAGYLAQAHİNNAAAİVAGKADVTSLG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 VHSPNESTLVVTLESPTSHFLKLLALPVFFPV--HKSQRTLQSKSLP---IASGAFYPKN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 IKQKQWIKLSKNPHYYNQSQVETKTITIHFIPDANTAAKLFNQGK--LNWQGPPWGERIP 268
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326
                                                                                                                                                                                                                                                                                                                                                     39 NIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFK 98
                                                                                                                                                                                                                                                                                                                                                                                    38 NNHSDPGTLDPQKVEENTAAQIVLDLFEGLVWMDG-EGQVQPAQAERWEILDGGKRYIFH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 LRTPATILIPPEVKGFSATIFDELQKPMSERVAMAKALLKQAGYDASHPLRFELFYNKYD 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGW 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : : | : : | : | | : | | LHEKTAI------ALSSEWKKWLGAQVILRIMEWKTYLDARRAGDFMLSRQSW 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 FADFADPWAFLTIFAYPSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETF 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 DATYNDASSFLNTLKSDSEENVGHWKNAQYDALLNQATQITDATKRNALYQQAEVIINQQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 WVVNEKITARKNPKYRDAQHTVLQQVEYLALDNSVTGYNRYRAGEVDLTW-----VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 QETLSNLQSK--GHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 RAKTADHILPTNIHSYP----EHQKQEMAQRQAYAKKLFKEA-----LEELQITAKD
                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                           DB 1; Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                       PUTATIVE BINDING PROTEIN YGIS.
BOF56723071A54EF CRC64;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                               EcoGene; EG13011; ygis.
EcoGene; EG13011; ygis.
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; FALSE_NEG.
Transport; Periplasmic; Signal; Complete protecme.
SIGNAL.
                                                                                                                                                                                                                                                                                      14.5%; Score 397.5; DB 1; 25.8%; Pred. No. 1.4e-20; iive 82; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periplasmic oligopeptide-binding protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 AA.
                                                                                                                                                                                                                                       60694 MW;
                                                                EMBL; U28377; AAA69188.1; -. EMBL; AE000384; AAC76056.1; -. HSSP; P06202; 1B52.
                                                                                                                                                                                                                                                                                                                     Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                         535
                                                                                                                                                                                                                                   SEQUENCE 535 AA;
                                                                                                                                                                                                                                                                                                       Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                      Query Match
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OPPA_HAEIN
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Query Match 12.9%; Score 354.5; DB 1; Length 514; Best Local Similarity 24.2%; Pred. No. 1.4e-17; Matches 128; Conservative 105; Mismatches 213; Indels 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
STRAIN-RD / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

R FleisChmann R.D. Adams M.D. White O. Clayton R.A. Kirkness E.F.,

R Kerlavage A.R., Bult C.J. Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

R Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

R Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.,

"Whole-genome random sequencing and assembly of Haemophilus

T influenzage Rd.",
                                                                                                                                                                                                                                           SIMILARITY).
SUBCELLULAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN.
18949C9617514A99 CRC64;
                                                                                                                                                                                                                         IT BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00496; SBP bac_5; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
Peptide transport: Transport; Periplasmic; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ATQEVSGIYAFALN--PIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFL---- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 IYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKL-KSAFWSNGDPLTAEDFIESWKQV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VDPATAAPYASYLSYLQVENAQDIIDGKKKPAELGVEXKDDYTFVVHTTNPVPYTVSXXT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 TENINKEPLANMKLREALASALDKEALVSTIFLGRAKTADHLL-PTNIH-----SYPEHQ 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITILLSLS----VVLQGCK--ESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 IALALSYSAQAVIVPEGTQLDEKQH-----IVINNGAEPQSFDPHKTEGVPESNVAYQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SATFLAIENPSTDVARYRAGDLDMTS--YG--LPPEQFAKLQKELPGEVYVTRTLGTYSY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 KQEMAQRQAYAKKLFKEA-----LEELQITAKDLEHLNLIFPVSS----SASSLL-VQ 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 HQSLLPLPXKV-VEKLGDAWVKENYVGNGAYKLANHIINEKIEFERNPLYWNDKETVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --KLLALPVFFPVHKSQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 TITIHFIPDANTAAKLFNQGKLNNQGPPWGERIPQETLSNLQSK--GHLHSFDVAGTSWL
                                                                                                                                                                                  Science 269:496-512(1995).
-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE OLIGOPEPTIDE
PERMEASE, A BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM, IT F
PEPTIDES UP TO FIVE AMINO ACIDS LONG WITH HIGH AFFINITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 370; DB 1; Length 541; 25.0%; Pred. No. 1.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97; Mismatches 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000914; SBP_bac_5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60906 MW;
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Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541
                                                                                                                                                                                                                                                                                                                                                                                                                                               P06202; 1B52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HI1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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395 LIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADFWAFLTIFAYPSGV 454
                                                               ---SRRAGRYDVARAGWNADYNQATTFGNYFLSNSSN 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Probable).
-!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95530630; Pubmed-7542800; Fletschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spridges T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Ghebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00496; SBP bac_5; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
Hypothetical protein; Transport; Membrane; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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PUTATIVE BINDING PROTEIN H10213.
N-ACYL DIGLYCERIDE (PROBABLE).
789188C4328BDEBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                461 NTAKYANPEYDKAMAESYAATDAEGRAKAYAKAEEILGKDYGIVPIFN 508
                                                                                                               455 PPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIEPIYH
                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Putative binding protein H10213 precursor.
                                                                                                                                                                                                                                                                                                                                514 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=RD / KW20 / ATCC 51907;
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514 PU
24 N-
58876 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
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                                                            416 LENOEWKTYID---
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                                                                                                                                                                                                                                                                                                                       Y213_HAEIN
P44572;
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20;

Gaps

83;

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EDYSLSSDGLTYTFKLK-SAFWSNGDPLTAEDFIESWKQVATQEVSGIYAFALNPIKNVR 142
                                                                          143 KIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVFFPVHKSQRTLQSKSLPIA 202
                                                                                                                                              157 AVLEKALPVESLGLFAENDRTLRIELDKASPYLPSMLAHVSLLPHY-----AKSTEIFIS 211
                                                                                                                                                                                                                                    260 GPPWGERIPQETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEAL 319
                                                                                                                                                                             SGAFYPKNIKQKQWIKLSKNPHYYNQSQV---ETKTITIHFIPDANTAAKLFNQGKLNWQ 259
                                                                                                                                                                                                        212 NGAYOLORQAENQHI-LITUPYYWAKEKVIFQOVKYOKISVDADLSDFDVYMNPKKVN-- 268
                                                                                                                                                                                                                                                            | :| | :| | :| | 309
                                                                                                                                                                                                                                                                                               320 VSTIFLGRAKTADHLLPTNIHSYPEHQ--KQEMAQRQAYAKKLFKE-ALEE-----LQIT 371
                                                                                                                                                                                                                                                                                                                -----SLNQTIAMRLNHQLSQSDLLRVENQGMSWQELQTARTKGDFQLIR 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Holtzapple B., Khouri H., Wolf A.M., Utterboxf T.R., Hansen C.L., Holtzapple B., Khouri H., Wolf A.M., Utterboxf T.R., Hansen C.L., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., "Complete genome sequence of a virulent isolate of Streptococcus
24 KESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQENNLSGNIEPALA 83
                                                                                                                                                                                                                                                                                                                                                                                                                   432 GGWFADFADFMAFLTIFAYPSGVPPYAINHKD-----FLEILQNIEQE---QDHQKRSE 482
                          40 QKNTQLESNRVELKRGVYSD-LTLQPWQAQSEEQTQLLRDLFEGLT-AYDVQGNLVPAVA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94328326, PubMed-8051706, Alloing G., de Philip P., Claverys J.-P., "Three highly homologous membrane-bound lipoproteins participate in oligopeptide transport by the Ami system of the Gram-positive strantonness manumania.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                         372 AKDLEHLNLIFPVSSSASSLLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFRYAKE 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligopeptide binding protein aliB precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae.";
J. Mol. Biol. 241:44-58(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=R800;
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NCBL_TaxID=1313;
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Q51933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
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ALIB_STRPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                            -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
Science 293:498-506(2001).
-!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR OLIGOPEPTIDES; PROBABLY AN OLIGOPEPTIDE BINDING PROTEIN.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLVQENNLSGNIEPALAEDYSLSSDGLTYTFKL-KSAFW--SNGD---PLTAEDFIESWK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 QVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHF------GVHSPNESTLVVTLE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 KPELYMNSKTLATILFPVNADFLKSKGDDFGKADPSSILYNGPFLMKALVSKSAIEYKKN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 PHYYNQSQV-----ETKTITIHFIPDANTAAKLFNQGKLNWQGPPWGERIPQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNYWDAKNVEVDDVKLIYIDGSDQESLERNFIAGAYTTARLFPNSS-SYEG-----IKE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 ILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSE----ISLVKHIYE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LVLGTGVLLSACGNSSTASKTYNYV-----YSSDPSSLNYLAENRAATSDIVANLVD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 ETLSNLQSKGHLHSFDVAGTSWLTFNINKFPLN---------NMKLREALA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LVSTIFLG-RAKTADHLLPTNIHSYPEHQK---- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 --QEMAQRQAYAKKLFKEALEELQITAKDLE---HINLIFPVSSSASSLLVQLIREGWKE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 DGQDPYYNPEKAKAKFAEAKKELE--AKGVQFPIHLDKTVEVTDKVGIQGVSSIKQSIES 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 SLGFAIPIVGKEFALLQADL--SSGNFS------LATGGWFADFADPMAFLTIFAYP 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 SPTSHFLKLLALPVFFPVH----KSQRTLQSKSLP---IASGAFYFKNIKQKQWIKLSKN
                                                                                                                                                                                                                                                                                                                                                                                                              OLIGOPEPTIDE-BINDING PROTEIN ALIB.
N-ACYL DIGLYCERIDE (PROBABLE).
A -> R (IN REF. 1).
SL -> HI (IN REF. 1).
LQ -> FE (IN REF. 1).
G -> E (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                            Peptide transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 12.3%; Score 337; DB 1; Length 65; Local Similarity 22.9%; Pred. No. 3.4e-16; nes 146; Conservative 119; Mismatches 218; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169B67FD78CFF0CF CRC64;
                                                                                                                                                                                                                                                                                       TIGR; SF152/;
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; I.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; I.
PROSITE; PS01040; SBP_BACTERIAL_5; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72562 MW;
                                                                                                                                                                                                                                                                   AE007448; AAK75616.1;
SP1527; -.
                                                                                                                                                                                                                                                     EMBL; 216082; CAA78896.1;
                                                                                                                                                                                                                                                                                                                                                                                              24
652
25
55
80
124
501
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                                                                                              PROTEIN FAMILY 5.
                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 AA;
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123 ATQEVSGIYAFALNPIKNVRKIQEGHLSIDHFGVHSPNESTLVVTLESPTSHFLKLLALP 182

55

---SKTELQITLKSAYYPFLQELALP 158

114 LDNRQRHAWLELANQIVDVKAL--

g δ

δ Q $Q_{\overline{Y}}$ q Qγ qq δλ g δy g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-RIZ / MG1655,
MEDLINE-94316500; PubMed-8041620;
SCATA H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.",
Nucleic Acids Rees. 22.2576-2586(1994).
-! FUNCTION: INVOLVED IN A NICKEL TRANSPORT SYSTEM, PROBABLY
REPRESENTS THE NICKEL BINDER.
-! SUBCELLOLAR LOCATION: Periplesmic (Probable).
-! SUBCELLOLAR LOCATION: Periplesmic (Probable).
-! SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
460 VLGSDNVVI---DIQQLISDEFDSSGYFAQTAAQKDYDLYHGGWGPDYQDPSTYLDIFNIN 517
                                   S------GVPPYAINHKD------FLEILQNIEQEQDHQKRSELVSQASLYLETFHII 497
                                                            518 SGGFLQNLGLEPGEANDKAKAVGLDVYTQMLEEANKEQDPAKRYEKYADIQAMLIDSSLV 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Navarro C., Wu E.-F., Mandrand-Berthelot M.-A.;
"The nik operon of Escherichia coli encodes a periplasmic binding-
protein-dependent transport system for nickel.";
Mol. Microbiol. 9:1181-1191(1993).
                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NICKEL-BINDING PERIPLASMIC PROTEIN. CB2E3C1CDCE42396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000423; AA775501.1; -.
PIR; S39584; S39594.
Brodene; E012075; nikA.
Interpro; IPRO00914; SSP_bac_5.
PROSITE; PS01040; SSP_BACTERIAL_5; 1.
Transport; Nickel; Signal; Periplasmic; Complete proteome.
                                                                                                     498 EPIYHDAFQFAMNKKL---SNLGVSPT-GVVDFRYAK 530
                                                                                                                                    578 LPSVSRGGTPSLRRTVPFAAAYGLTGTKGVESYKYLK 614
                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Nickel-binding periplasmic protein precursor.
                                                                                                                                                                                                                                  524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE~95020649; PubMed~7934931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58719 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00039; AAB18451.1; -.
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                               NIKA OR B3476
                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
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SERAIN-ED / KWA20 / ATCC 51907;
STRAIN-ED / STRAIN-ED / White O., Clayton R.A., Kirkness E.F.,
STRAIN-ED / SUtton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
STRAIN-ED / Shirley R., Liu L.-I., Gloddek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Chebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                    type b encodes a heme-dependent Haemophilus
                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heme-binding protein A precursor (Hemin-binding lipoprotein).
                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C., "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                       547 AA.
                                                                                                                                                                                                                                                                                       Hanson M.S., Slaughter C., Hansen E.J.; "The hbpA gene of Haemophilus influenzae heme-binding lipoprotein conserved among
                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                             Infect. Immun. 60:2257-2266(1992).
                                                                                                                                                                                                                                                         STRAIN=DL42 / SEROTYPE B;
MEDLINE=92267636; PubMed=1339409;
                                                              01-FEB-1994 (Rel. 28, Created)
                                     STANDARD;
                                                                                                                                                        Haemophilus influenzae
                                                                                                                                                                                                        NCBI_TaxID=727;
                                                                                                                                                                                          Haemophilus.
                                  HBPA_HAEIN
P33950:
                                                                                                                                                                                                                                                                                                                                                 species.
RESULT 11
HBPA_HAEIN
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11.0%; Score 301; DB 1; Length 524; 24.2%; Pred. No. 8.4e-14;

Local Similarity 24.2%; Pred. No. 8.4e-14; hes 119; Conservative 93; Mismatches 209; Indels

18;

70;

Query Match

Matches

Science 269:496-512(1995),

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                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                            PROBABLE.

HEME-BINDING PROTEIN A.

N-ACYL DIGLYCRENDE (PROBABLE).

KA -> NS (IN STRAIN D142).

T -> N (IN STRAIN D142).

T -> I (IN STRAIN D142).

T -> I (IN STRAIN D142).

A -> V (IN STRAIN D142).

A -> V (IN STRAIN D142).

A -> V (IN STRAIN D142).
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Pfam; PF00496; SBP_bac_5; 1.
PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01040; SBP_BACTERIAL_5; 1.
Inner membrane; Signal; Lipoprotein; Complete proteome.
                                                         POSSIBLE FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M88134; AAA73214.1; ALT_SEQ.
EMBL; W84028; AAA24962.1; -
EMBL; U32767; AAC22512.1; ALT_INIT.
                                                                                     STRAIN=DL42 / SEROTYPE B;
MEDLINE~91251755; PubMed=2041470;
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49
181
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                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN FAMILY 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A43832; A43832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P23847; 1DPE.
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19
181
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343
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LIPID
VARIANT
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VARIANT
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18;
                                                                                                                               62 KHIYEGLVQENNLSGNIEPALAEDYSLSSDGLIYTPKLKSA-----FWSNGDPLTAE 113
                                                                                                                                                             69 QOVYNRLVEFKKGSTDIEPALAESWEISDDGLSYTFHLRKGVKFHTTKEFTPTRD-FNAD 127
                                                                                                                                                                                                                   168
                                                                                                                                                                                                                             DVVFSFQRQLDPN-----HPYHNVSKGTYPYFKAMKFPELLKSVEKVDDNTIRITL 178
                                                                                                                                                                                                                                                                                                179 NKTDATELASLGMD-FISIYSAEYADSMLKAGKPETLDSR--PVGTGPFVFVDYKTDQAI 235
                                           Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                      273
                                                                                                                                                                                                                                                                                                                                                         236 GYVAHENYW-KGRTPLDRLVISIVPDATTRYAKLQAĞTCDLILFPNVADLAKMKTDPKVQ 294
                                                                                                                                                                                                                                                                                                                                                                                                   274 NLQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADH 333
                                                              13 LLSLSVVLQGCKESSHS-----STSRGELAINIRDEPRSLDPRQ-VRLLSEISLV 61
                                                                                            9 LAAATLVLAACDQSSSANKSTAQTEAKSSSNNTFVYCTAKAPLGFSPALIIEGTSYNASS 68
                                                                                                                                                                                                                                                                                                                                                                                                                       114 DFIESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHF-----GVHSPNESTLVVTL
                                                                                                                                                                                                                                                                                                                                   KLSKNPHYYNQSQVETKTITIHFIPDANTAAKLFNQGKLNW-QGPPWGERIPQET---LS
                                                                                                                                                                                                                                                                169 ESPTSHFLKLLALPVFFPVHKSQ------RTLQSKSLPIASGAFYPKNIKQKQWI
            DB 1; Length 547;
   10.6%; Score 291.5; DB 1; 23.1%; Pred. No. 4.2e-13; tive 95; Mismatches 259;
                                    Conservative
                   Similarity
                                 128:
Query Match
Best Local S
Matches 128
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EMBL; AE000245; AAC74560.1; -.
EMBL; D90789; BAA15142.1; ALT_INIT.
EMBL; D90790; BAA15152.1; ALT_INIT.
EMBL; D90791; BAA15158.1; ALT_INIT.
ECOGENE; EG13790; YddS.

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334 LLPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEELQITAKDLEHLNLIFPV---SSSASS 390
                               348 PLPPTIWSYND-EIQDYPYDPEKAKQLLAEA----GYPNGFETDFWIQPVIRASNPNPK 401
                                                                                                      402 RMAELIMADWAK-IGVKTNPVTYEWADYRKRAKEGELTAGIFGWSGDNGDPDNFLSPLLG 460
                                                                                                                                                                 | : | . : | . : | . | . | . | . | 461 SSNIGNSNMARPNNSEFDALLNEAIGLTHKEERAKLYKQAQVIVHNQAPWIPVAHSVGFA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Periplasmic (Potential).
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                     YDDS_ECOLI STANDARD; PRT; 516 AA.
PF6458, P7769; P7684; P7684.
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative ABC transporter periplasmic binding protein yddS precursor.
YDDS OR B1487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alba H., Baba T., Fujila K., Hayashi K., Inada T., Isono K., Kitagawa M., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miwi T., Mizobuchi K., Mori H., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Yanamoto Y., Horiuchi T., Takeda J., Takemoto K., Takeuchi Y., Mada C., "A 570-kb DNA sequence of the Escherichia coli K-12 genome Corresponding to the 28.0-40.1 min region on the linkage map."; PUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                    391 LLVQLIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADFMAFLTIFAY
                                                                                                                                         451 PSGV---PPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIEPIYHDAFQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                              508 AMNKKLSNLGVSPTG 522
                                                                                                                                                                                                                                          521 PLSPRVKGYVQSPFG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                      YDDS ECOLI
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20;
                                                                                                                                                                                                                                 NNLSGNIEPALAEDYSLSSDGLTYTFKLK-SAFWSNGDPLTAEDFIESWKQVATQEVSGI 130
                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                              131 YAFALNPIKNVRKIQEG-----HLSIDHFGVHSPNESTLVVTLESPTSHFLKLLA--- 180
                                                                                                                                                                                                                                                                                                                                                    168 ASIINPAVLKEHAADDARGFLAQNT-----AGSGPFMLKSWQKGQQLVLVPNPHYPG- 219
                                                                                                                                                                                                                                                                                                     -----KIGGGPAEAFPKDLKID-----APDEHTVKFTLSOPFAPFLYTLANDG 167
                                                                                                                                                                                                                                                                                                                                                                            SQVETKIIITHFIPDANTAAKLFNQGKLNWQGPPWGERIPQETLSNL--QSKGHLHSFDV 286
                                                                                                                                                                        Gaps
                                                                                                                                                                                 16 LSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIXEGLVQ----E 71
                                                                                                                                                                                                          LALVLATNFPVAHAAVPKDMLVIGKAADPQTLDPAVTIDNNDWTVTYPSYQRLVQYKTDG 71
                                                                                                                                                                                                                                                                                                                                                                                                                             287 AGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHLLPTNIHSYPEHQ 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 KQEMAQRQAYAKKLFKEALBELQITAKDLEHLNLIF------PVSSSASSLLVQLIRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 QMKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWPADFADPMAFLTIF--AYPSGVPP 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last Sequence update)
Last annotation update)
transport protein precursor (Dipeptide-binding
                                                               POTENTIAL.
PUTATIVE ABC TRANSPORTER PERIPLASMIC BINDING PROTEIN YDDS.
                                                                                                                                                                                                                                                                                                                               181 ----LPVFFPVHK-----SQRTLQSKSLPIASGAFYPKNIKQKQWIKLSKNPHYYNQ
                                                                                                                                                                                                                                                   275 LRVTYLYLMNSKAPLNOADLRRAISWSTDYQGMYNGILSGNGKQMRGPIPEGHWGYD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ATAMQYNHDETKAKAEWDKVTSKPTS-LTFLYSDNDPNWEPIALATQSSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457 YAINHKDFLE----ILQN-----IEQEQDHQKRSELVSQASLYLETFHIIEPIYHD
                                                                                                                                                                   Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                             Length 516;
                                                                                                     86E1C32CC3E06FB9 CRC64;
            Pfam; PF00496; SBP_Jac_5, 1.

PROSITE; PS01040; SBP_BACTERIAL_5; 1.

Hypothetical protein; Transport; Periplasmic; Signal; Complete proteome.
                                                                                                                                            DB 1;
                                                                                                                                                             Conservative 109; Mismatches 208;
                                                                                                                                       10.5%; Score 287.5; DB 1
22.1%; Pred. No. 7.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 AA.
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 IPR000914; SBP_bac_5.
                                                                                                 57641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFQFAMNKKLSNLGVSP 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487 NYQLAMNKEVKGFVFNP 503
                                                             25
516
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Periplasmic dipeptide
                                                                                                 516 AA;
                                                                                                                                                 Similarity
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DPPA OR B3544.
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                                                                                                                                                          Matches 123;
  InterPro;
                                                                                               SEQUENCE
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                                                                                                                                    Query Match
                                                                                                                                                  Local
                                                             SIGNAL
                                                                        CHAIN
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DPPA_EC
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                                                                                                                               MEDLINE=92065799; PubMed=1956284;
Abouhamad W.N., Manson M., Gibson M.M., Higgins C.F.;
"Peptide transport and chemotaxis in Escherichia coli and salmonella typhimurium: characterization of the dipeptide permease (Dpp) and the dipeptide-binding protein.";
Mol. Microbiol. 5:1035-1047(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- FUNCTION: DIPERTIDE-BENDING PROTEIN OF AN OSMOTIC-SHOCKABLE TRANSPORT SYSTEM. DPPA IS ALSO REQUIRED FOR PEPTIDE CHEMOTAXIS.
-:- SUBCELLUIAR LOCATION: Periplasmic.
-:- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               properties of proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunten P., Mowbray S.L., "Crystal structure of the dipeptide binding protein from Escherichia coli involved in active transport and chemotaxis."; Protein Sci. 4:2327-2334(1995).
                                                                                                                                                                                                                                                                                                         Abounamed W.N., Manson M.D., The dipeptide permease of Escherichia coli closely resembles other
                                              coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F. Analysis of the Escherichia coli genome. V. DNA sequence of the
            Olson E.R., Dunyak D.S., Jurss L.M., Poorman R.A.; "Identification and characterization of dppA, an Escherichia gene encoding a periplasmic dipeptide transport protein."; J. Bacteriol. 173:234-244(1991).
                                                                                                                                                                                                                                                                                                                                           bacterial transport systems and shows growth-phase-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "2-A resolution, tructure of DppA, a periplasmic dipeptide transport/chemosensory receptor.";
Blochemistry 34:16585-16595(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the SWISS-PROT data bank.
                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 29-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96118375; PubMed-8527431;
Nickitenko A.V., Trakhanov S., Quiocho F.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Link A.J., Robison K., Church G.M., "Comparing the predicted and observed profin the genome of Escherichia coli K-12.", Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 14:1077-1092(1994).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-K12 / MM500;
MEDLINE-95231288; PubMed=7536291;
MEDLINE=91100289; PubMed=1702779;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94316500; PubMed=8041620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
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STRAIN-K12 / MG1655;
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SEQUENCE OF 29-40.
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us-09-824-567-2.rsp

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TIGE;
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            20;
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                                                                                                                                                                                                                                                             117 ESWKQVATQEVSGIYAFALNPIKNVRKIQEGHLSIDHF-GVHSP-----NESTLVV 166
                                                                                                                                                        PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                        120 FSFDRQKN-----AQNP---YHKVSGG--SYEYFEGMGLPELISEVKKVDDNTVQF 165
                                                                                                                                                                                                                                                                                                                           167 TLESPTSHFLKLLALPVFFPVHKSQRTLQSKS-----LPIASGAFYPKNIKQKQWIK 218
                                                                                                                                                                                                                                                                                                                                               166 VLTRPEAPFLADLAMDFASILSKEYADAMMKAGTPEKLDLNPIGTGPFOLQQYQKDSRIR 225
                                                                                                                                                                                                                                                                                                                                                                                  226 YKAFDGYWGTKPQIDTLVFSI--TPDASVRYAKLQKNECQVMPYPNPADIARWKQDKSIN 283
                                                                                                                                                                                                                                                                                                                                                                219 LSKNPHYY-NQSQVETKTITIHFIPDANTAAKLFNQGK---LNWQGPPWGERIPQETLSN 274
                                                                                                                                                                                                                                                                                                                                                                                                     275 LQSKGHLHSFDVAGTSWLTFNINKFPLNNMKLREALASALDKEALVSTIFLGRAKTADHL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                          335 LPTNIHSYPEHQKQEMAQRQAYAKKLFKEALEELQITAKDLEHLNLIFPVSSSASSLLVQ 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 LIREQWKESLGFAIPIVGKEFALLQADLSSGNFSLATGGWFADFADP-MAFLTIF---AY 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIQADWAK-VGVQAKIVTYEWGEYLKRAKDGEHQTVMMGWTGDNGDPDNFFATLFSCAAS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 PSGVPPYAINHKDFLEILQNIEQEQDHQKRSELVSQASLYLETFHIIEP---IXHDAFQF
                                                                                  EcoGene; EG10Z40; Lrr...
InterPro; IPR000014; SBP_bac_5.
InterPro; IPR000014; SBP_bac_5.
PROSITE: PS01040; SBP_BACTERIAL_5; 1.
PROSITE: PS01040; SBP_BACTERIAL_5; 1.
Peptide transport; Transport; Periplasmic; Signal; Chemotaxis; 3D-structure; Complete proteome.
PERIPLASMIC DIPEPTIDE TRANSPORT F
                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                               Score 283.5; DB 1; Length 535; Pred. No. 1.5e-12;
                                                                                                                                                                                                           10.4%; Score 20.1.;
24.6%; Pred. No. 1.5e-12;
**ive 85; Mismatches 223; Indels
                                                                                                                                                                                  60293 MW; 3F7C4756EEA8C2F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P18791; P18792; 01-NOV-1990 (Rel. 16, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
01igopeptide-binding protein amiA precursor.
Streptococcus pneumoniae.
                                                                         ECO2DBASE; G059.9; 6TH EDITION. EcoGene; EG10248; dppA.
                    : AE000431; AAC76569.1; -. S15292; S15292.
L08399; AAA23702.1; ...
U00039; AAB18522.1; -.
                                              PDB; 1DPE; 17-AUG-96.
PDB; 1DPP; 07-DEC-95.
SWISS-2DPAGE; P23847; COLI.
                                                                                                                                                                                                           Query Match
Best Local Similarity 24.69
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 PVRKEVKGYVVDPLG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 AMNKKLSNLGVSPTG 522
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                                       A39194; A39194.
                                                                                                                                                              34 2
450 4
535 AA;
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P18791; P18
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                    EMBL;
                             PIR;
PIR;
PDB;
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ID AMIA_S
AC P18791
DT 01-8791
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DT 16-0CT
DF 01gook
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OS Streptc
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                                                                                                                                                                                                                                 Alloing G., Trombe M.C., Claverys J.-P.; The ami locus of the Gram-positive bacterium Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rmatics and the EMBL outstation
There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Unrish A.S., Gwinn M., Rolonay J.E., Nelson W.C., Peterson J.D., Unayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., Hochald L.A., Feldhlyum T.V., Angiuoli S., Diokinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin B., Alloing G., Boucraut C., Claverys J.-P.;
"The difficulty of cloning Streptococcus pneumoniae mal and ami loci
in Escherichia coli: toxicity of malx and amiA gene products.";
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR OLIGOPEPTIDES; PROBABLY AN OLIGOPEPTIDE BINDING PROTEIN.
-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: THE REVISED SEQUENCE OF AMIA NOW INCLUDES, IN THE C-TERMINAL SECTION, THE SEQUENCE OF AN ORP WHICH WAS PREVIOUSLY
                                                                                                                                                                                                                                                                                                       is similar to binding protein-dependent transport operons of gram-negative bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Evidence for high affinity binding-protein dependent transport systems in Gram-positive bacteria and in Mycoplasma."; EMBO J. 7:3971-3974(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gilson E., Alloing G., Schmidt T., Claverys J.-P., Dudler R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claverys J.-P.;
Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                      STRAIN=R800;
MEDLINE=90279506; PubMed=2352474;
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MEDLINE=89091147; PubMed=3208757;
                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 4:633-644(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 293:498-506(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 80:227-238(1989).
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                                                                                                                                       SEQUENCE FROM N.A.
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                                                                        NCBI_TaxID=1313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS.
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26;
                                                                                                                                                                                                                                                                                                                                 59 SLVKHIYEGLVQENNLSGNIEPALAEDISLSSDGLTYTFKLKSA---FWSNGD---PLTA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                172 TSHFLKLLALPVFFPVHKSQRTLQSKSLP-----IASGAFYPKNIKQKQWIKLSKNP 223
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                                               PROBABLE.
OLIGOPEPTIDE-BINDING PROTEIN AMIA.
                                                                         N-ACYL DIGLYCERIDE (PROBABLE).
S -> R (IN REF. 1).
A -> R (IN REF. 1).
R -> K (IN REF. 1).
L -> F (IN REF. 1).
S -> L (IN REF. 1).
V -> A (IN REF. 1).
W -> A (IN REF. 1).
PS01040; SBP_BACTERIAL_5, 1.
Transport; Transport; Signal; Membrane; Lipoprotein;
                                                                                                                                                                                                                            DB 1; Length 659;
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                                                                                                                                                                                                                                      llarity 21.6%; Pred. No. 7.3e-12;
Conservative 107; Mismatches 255;
                                                                                                                                                                                                                      10.1%; Score 275.5; 21.6%; Pred. No. 7.3¢
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             Peptide transport;
Complete proteome.
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Uburkin A.S., Gwinn M., Kolonay J.E., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.R., Fraser C.M., Compolete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Probable).
-:- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                      Alloing G., de Philip P., Claverys J.-P.,
"Three highly homologous membrane-bound lipoproteins participate in
oligopeptide transport by the Ami system of the Gram-positive
etrephococus pneumoniae.";
   Streptococcus pneumoniae.
Bacteria, Firmicutes, Bacillus/Clostridium group, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                Coffey T.J., Enright M.C., Daniels M., Morona J.K., Morona R., Hrynlewicz W., Paton J.C., Spratt B.G.; Recombinational exchanges at the capsular polysaccharide biosynthetic locus lead to frequent serotype changes among natural isolates of Streptococcus pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR MOIL MICEODIOL, 9:1037-1050(1993).
-I- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SY
FOR OLIGOPEPTIDES; PROBABLY AN OLIGOPEPTIDE BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pearce B.J., Yin Y.B., Masure H.R., "Genetic identification of exported proteins in Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pearce B., Naughton A.M., Masure H.R.; "Peptide permeases modulate transformation in Streptococcus
                                                                                                                                                                                                                                   STRAIN-NCTC 11906, SP-496, SP-VA92, AND SP-VA96,
MEDLINE-98125733; PubMed-9466257;
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                                                                                                            MEDLINE-94328326; PubMed=8051706;
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MEDLINE=95020610; PubMed=7523829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95020625; PubMed=7934910;
                                                                                                                                                                          Streptococcus pneumoniae.", J. Mol. Biol. 241:44-58(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 18-660 FROM N.A.
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                                Streptococcus.
NCBI_TaxID=1313;
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EMBL; 235135; CAA84507.1; -.
EMBL; AE007348; AAK74534.1; ALT_INIT.
EMBL; AF030359; AAC38676.1; -.
EMBL; AF030360; AAC38681.1; -.

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OLIGODEPTIDE-BINDING PROTEIN ALIA.

N-ACYL DIGLYCERIDE (PROBABLE).

F -> L (IN STRAIN R800).

G -> D (IN STRAIN SOUTC 11906, SP-VA92,
SP-496 AND SP-VA96).

T -> A (IN STRAINS R800 AND R6X).

E -> D (IN STRAINS R800 AND R6X).

SP-496 AND SP-VA96).

L -> I (IN STRAINS R800 AND R6X).

L -> I (IN STRAINS R800, R6X, NCTC 11906, SP-VA92, APPS P496 AND SP-VA96).

C -> T (IN STRAINS NCTC 11906, SP-VA92, APPS P496 AND SP-VA96).

T -> A (IN STRAINS NCTC 11906, SP-VA92, SP-VA96 AND SP-VA96).

T -> A (IN STRAINS RPC 11906, SP-VA92, SP-VA96 AND SP-VA96).

T -> A (IN STRAIN SP-VA96).

T -> A (IN STRAIN SP-VA96).

T -> C (IN REF. 4).

A -> R (IN REF. 4).

A -> R (IN REF. 1).

MW; 702556P92EC055E8 CRC64;
                                                                               Peptide transport; SBP_BACTERIAL_5; 1. Complete proteome: Transport; Membrane; Lipoprotein; Signal; SIGNAL ...
                                           InterPro: IPR000914; SBP_bac_5.
Pfam: PF00496; SBP_bac_5; 1.
PROSITE: PS00013; PROKAR_LIPOPROTEIN: 1.
PROSITE: PS01040; SBP_BACTERIAL_5; 1.
  AF030361; AAC38686.1; -. AF030364; AAC38703.1; -. L20556; AAA26952.1; -. SP0366; -.
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24; 72 NNLSGNIEPALAEDYSLSSDGLTYTFKL-KSAFW--SNGD---PLTAEDFIESWKQVATQ 125 Query Match
9.9%; Score 272.5; DB 1; Length 660;
Best Local Similarity 21.4%; Pred. No. 1.2e-11;
Matches 128; Conservative 105; Mismatches 229; Indels 137; Gaps 126 EVSGIYAFALNPIKNVRKIQEGHL-SIDHFGVHSPNESTLVVTLESPTSHFLKLLALPVF 184 131 KSDALY-LVQESIKGLDAYVKGEIKDFSQVGIKALDEQTVQYTLNKPESFWNSKTIMGVL 189 185 FPVHKSQRTLQSK-----SLPIASGAFYPKNIKQKQWIKLSKNPHYYNQSQVETK 234 272 L----SNLQSKGHLHSFDVAGTSMLTFNINKFPLNNKKLREALASALDKEALVS----- 321 302 ITYLVGTNIDRQSYKYT---SKTSDEQKASTKKALLNKDFRQAIAFGFDRTAYASQLNGQ 358 359 TGASKILRNLFVPPTFVQADGKNFGDMVKEKLVTYGDEMKDVNLADSQDGLYNPEKAKAE 418 12 ILLSLSVVLQGCKESSHSSTSRGELAINIRDEPRSLDPRQVRLLSEISLVKHIYEGLVQE 71 12 VTLLAATTLAACSGSGSSTKGEKTFSYIYETDPDNLNYLTTAKAATANITSNVVDGLL-E 70 248 KVKLSFWDGQDTSKPAENFKDGSLT-----AARLYPTSASFAELEKSMKDNIVYTQQDS 301 322 ------QEMAQRQAYAKKL 360 | :| || |: :: ::| || :|: :| || 419 FAKARSALQ--ABGVQFPIHLDMPVDQRATTRVQRVQSMKQSLEATLGADNVIIDIQQLQ 476 ----- 445 -----PQET 477 KDEVNNITYFAENAAGEDW-----DLSD-----NVGWGPDFADPSTYLDIIKPSVGEST 361 FKEALEELQITAKDLEH-LNLIFPVSSSASSLL--VQLIREQWKESLG-----------FAIPIVGKEFALLQADLSSGNFSLATGGWFADFADPMAFL----235 TITIHFI--PDANTAAKLFNQGKLNWQGPPWGERI-----406 ò q ŏ g δy g δ QQ δŽ g ŏ g g 8 Qγ q

Search completed: July 26, 2002, 04:42:32 Job time: 260 sec

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July 26, 2002, 04:36:22; Search time 87.81 Seconds (Without alignments) 1048.096 Million ceil updates/sec
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2739
1 MRKISVGICITILLSLSVVL.....LSNLGVSFTGVVDFRYAKEN 532
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                       OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

Sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

sp_rodent:*
sp_virus:*
sp_vertebrate:*

sp_plant:*

| | Description | | 094201 chlamydia p | | | | _ | Q9K244 chlamydia p | O9pkl9 chlamydia m | 084178 chlamydia t | | Q9k5f7 borrelia ga | 09k5j9 borrelia af | 031305 borrelia bu | | | ~ . | Vazano listeria in |
|-----------|--------------------------|--------|--------------------|---------|----------|-------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|
| SUMMARIES | ID | 6X8Z6O | 084201 | 09PK,74 | 2097.8VR | 94860 | 010373 | 00000 | 084179 | 0/1#00 | Q9/D40 | C3V3F7 | 20000 | 001700 | 004084 | 003400 | 0929H6 | |
| | | 16 | 16 | 16 | 16 | 16 | 1 1 | 9 4 | 9 4 | 9 4 | 2 6 | 4 0 | 40 | 4 - | 2 4 | 4 | 19 | |
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| ж | Query Match | 100.0 | 49.8 | 49.1 | 42.4 | 27.6 | 27.6 | 27.3 | 25.0 | 19 | 8 6 | 18.0 | | 20.00 | 17.6 | 17.5 | 17.5 | |
| | Score | 2739 | 1364 | 1345 | 1160.5 | 755.5 | 755.5 | 748 | 685.5 | 536.5 | 509.5 | 506 | 505.5 | 505.5 | 482.5 | 479.5 | 478 | |
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| Q93QH8 Q9LAT7 Q9CIL3 Q31315 Q53480 | 092784 098506 097048 098134 098888 0988114 | 031303 050927 050927 052615 052615 051307 092FA6 084141 | 051308 09PKP9 09C127 031304 031306 083594 051643 |
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| | | PRT: 532 AA | | Created | Last sequence undate: | Last apportation undate: | N | | vdophila phenmoniae. | BENGLACES CHISTIAN CONTROL OF THE CO | maracac, ciramyoopiira. | | | | 192388: | athe B Tammel C Bar # | Olinger L., Grimwood I. Davie B E stemper P. Hyman K.W., | "Comparative genomes of Chlamatism, occurrence K.S.; | "Tara puediloniae and c. trachomatis. | <u>.</u> | |
| NECOLUL 1 | 0928Y9 | | | | (TrEMBLrel. 10, Last Sequence undate) | "01 DEC 2001 (TrEMBLrel, 19, | OLIGOPEPTIDE BINDING PROTEIN | OPPA_1 OR CPN0195 OR CP0572. | Chlamydia pneumoniae (Chlamydophila pneumoniae) | Bacteria; Chlamydiales: Chlamydiaceae: Chlamydiaceae | NCBI_TaxID=83558; | [1] | SEQUENCE FROM N.A. | STRAIN-CWL029; | MEDLINE=99206606; PubMed=10192388. | Kalman S., Mitchell W. Mar | Olinger L., Grimwood T. Day | "Comparative genomes of chi | Nat. Genet. 21:385-389(1999) | [2] | ייי ייי ייי ייי ייי ייי ייי |
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ALIGNMENTS

MEDINE-2015025; PubMed-10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Eisen J., Fraser C.M., Eisen J., McClarty G., Salzberg S.L., Cenome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39."; SEQUENCE FROM N.A. SEQUENCE FROM N.A.

STRAIN-J138;
MEDLINE-20330349; PubMed-10871362;
Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138

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                                                                                            58858 MW; 8B3AE840831BBEF1 CRC64;
                                                                                                                                 1 49.8%; Score 1364; DB 16; Similarity 50.1%; Pred. No. 9.8e-94; 59; Conservative 97; Mismatches 147;
                     Science 282:754-759(1998).
EMBL; AE001293; AAC67790.1; -.
InterPro; IPR000914; SBP_bac_5.
Pfam. PF00496; SBP_bac_5; 1.
Complete proteome.
SEQUENCE 518 AA; 58858 MW; 8B
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            Chlamydia trachomatis.";
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                                                                                                                                                                                                                                                                                                                                         VKHIYEGLVQENNLSGNIEPALAEDYSLSSDGLTYTFKLKSAFWSNGDPLTAEDFIESWK 120
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SEQUENCE 532 AA; 59744 MW; 1CB473D9D46A1579 CRC64;
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Pred. No. 1.5e-196;
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Last sequence update)
Last annotation update)
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NCBI_TaxID=813;
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from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
EMBL, AE0016.6; AAD18348.1;
EMBL, AE00216; AAR38391.1;
EMBL; A2002245; BAR98405.1;
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                                                                                            Pfam; PF00496; SBP_bac_5; 1.
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Best Local Similarity 100.C
Matches 532; Conservative
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SEQUENCE FROM N.A.
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STRAIN=MOPN / NIGG,
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Halkeye B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Elsen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
476 DHQKRSELVSQASLYLETFHIIEPIYHDAFQFAMNKKLSNLGVSPTGVVDFRYAKEN 532
                                 PROTEIN,
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-0BC-2001 (TrEMBLrel. 19, Last annotation update)
PEPTIDE ABC TRANSPORTER, PERIPLASMIC PEPTIDE-BINDING
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID-83560;
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Matches 79, Conservative
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'COATION: (114)...(713)

'NAME/KET: sig_peptide

'LOCATION: (21)...(113)

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LENGTH: 914
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Sequence 57, A
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Sequence 63, A
Sequence 3, Ap
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-245-511-46
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US-08-356-340-3
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US-08-356-340-3
US-08-3746-3-14
US-08-3746-3-14
US-08-31-860-5
US-09-31-860-5
US-09-450-852-3
US-09-450-852-3
US-08-378-588-5
US-08-378-588-5
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US-08-38-829-887-8
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Pred. No. 0.017;
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US-08-590-399-11
US-08-913-159-12
US-08-913-159-12
US-08-913-59-4
US-08-08-255-6
US-08-08-255-6
US-08-08-713-6
PCT-US-91-0585-6
US-09-265-315-52
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Patent No. 6350604

GENERAL INFORMATION:
APPLICANT: Hirayama, Satoshi
APPLICANT: Taira, Rikako
APPLICANT: Bandal, Thomas
APPLICANT: Bondal, Thomas
APPLICANT: Bandal, Thomas
APPLICANT: Genboll, Karen M.
APPLICANT: Oxenboll, Karen M.
APPLICANT: Displayine Lipolytic Enzyme
FILE OF INVENTION: Alkaline Lipolytic Enzyme
CURRENT ENERGENE: 4698 204-15
CURRENT FILING DATE: 1998-10-22
EARLIER FILING DATE: 1996-04-25
EARLIER FILING DATE: 1996-04-25
EARLIER FILING DATE: 1996-04-25
EARLIER APPLICATION NUMBER: 501/96
EARLIER FILING DATE: 1996-04-25
EARLIER PILING DATE: 1996-04-25
EARLIER APPLICATION NUMBER: 501/96
EARLIER FILING DATE: 1996-04-25
EARLIER FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 ttcaagaaaataatctttcaggaaatatagagcctgctcttgcagaagactactcttt 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%; Score 39; DB 2; Length 2019;
65.5%; Pred. No. 0.053;
tive 0; Mismatches 30; Indels
                                                                                                                                APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SER-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 cctcggacggactcacttatactttta 392
                                                         Sequence 46, Application US/08245511
Patent No. 5928900
GENERAL INFORMATION:
                                                                                                                                                                                                                                     SEE: Klauber & Jackson
: 411 Hackensack Avenue
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201313-1684
TELEX: 1352343-1684
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 2019 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                          APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Conservative
                                                                                                                                                                                                                                                                                           New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..1932
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Str
                                                                                                                                                                                                                                                                                      STATE: New COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R6
                                                                                                                                                                                                                                 ADDRESSEE:
                      RESULT 2
US-08-245-511-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-245-511-46
                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                            APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Blaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/M
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Sequence 46, Application US/08600993A; Patent No. 5981229; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REPERSOMMURENCE/DOCKET NUMBER: 600-1-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELERX: 13521
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2019 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: SPRU98
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GENERAL INFORMATION:
APPLICANT: FROMMER, Wolf-Bernd
APPLICANT: RIESBEIER, Dorg
TITLE OF INVENTION: DASAMINS, BACTERIA AND PLANTS CONTAINING A TRANSPORTER,
TITLE OF INVENTION: PLASMINS, BACTERIA AND PLANTS CONTAINING A TRANSPORTER
TITLE OF INVENTION: AS WELL AS A PROCESS FOR PREPARATION AND TRANSFORMATION
TITLE OF INVENTION: OF YEAST STRAINS FOR THE IDENTIFICATION
              1486 ACTCACAATGTTGCCATCTCCACCTGCTGATGCTAAGCCAGCAGTC-GCCATGGGGCTTT 1544
                                                     1492 cctagaaattctacaaaacatagaacaagagcaagatcaccaaaaacgctcggaattagt 1551
                                                                                             1545 CCATTAAATAATTACAAAAGAAGGAGGAACAACTTTTTTTAATATTAGTACTTCTCT 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1372 agggaacttctctttagctacaggaggatggttcgcagactttgctgatcctatggcatt 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1426 aggaaacttgcctggatttgtagttggagcagttgcagctgccgcgagcgctgttttagc 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1432 totaacgatotttgottatocatcaggagttcottcttatgcaatcaaccataaggactt 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1492 cctagaaattctacaaaacatagaacaagagcaagatcaccaaaaacgctcggaattagt 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1545 ccattaaataattacaaaagaaggagaagaagaacaactttttttaatattagtacttctct 1604
                                                                                                                                      1552 gtcgcaagcttctctttacctagagacctttcatattattgagccgatct 1601
                                                                                                                                                             Length 1773;
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Pred. No. 0.18;
0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/786,555B
CURRENT FILING DATE: 1997-01-21
EARLIER APPLICATION NUMBER: 08/356,340
EARLIER APPLICATION NUMBER: 08/356,340
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1993-06-22
EARLIER FILING DATE: 1993-06-22
MUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08786555B Patent No. 5981181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OKGANISM: Spinacia oleracea
US-08-786-555-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1773
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US-08-232-463-14
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                                                                                                                                                                                                                           JR, JOTG
DNA SEQUENCES WITH OLIGOSACCHARIDE
TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A
TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND
TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1372 agggaacttctctttagctacaggaggatggttcgcagactttgctgatcctatggcatt 1431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1432 tetaaogatetttgettatecateaggagtteeteettatgeaateaaceataaggaett 1491
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0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,340
FILING DATE: 21-DEC-1994
CLASSIFICATION: 800
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 5.1552
OTHER INFORMATION: /note= "Sucrose-Transporter"
                                                                                                                                                                                                                                                                                                                                                                      1: Ostrolenk, Faber, Gerb & Soffen
1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/EP93/01604
FILING DATE: 22-JUN-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 94 2 20 759.2
FILING DATE: 24-JUN-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
P/951-106
                                                                                                                                          Sequence 3, Application US/08356340 Patent No. 5608146 GENERAL INFORMATION:
                                                                                                                                                                                                          Wolf-Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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TELEFAX: (212) 382-0888
TELEX: 236225
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1773 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PT TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meilman, Edward A. REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.4%;
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Best Local Similarity 50.4
Matches 116; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                      APPLICANT: FROMMER, WARPLICANT: RIESMEIER,
                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 10036-8403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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ORIGINAL SOURCE:
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                                                                                                  RESULT 4
US-08-356-340-3
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                                                                                                                    OPERATING SISTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELECOMONICATION INFORMATION:
TELEPHONE: (703)836-9300
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                               APPLICATION NUMBER: US/08/232,463
                                                      ZIP: 22313-025,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
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STRANDEDNESS: single
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            Alexandria
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Matches 22; Conserv
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                                                                                                         Human RAD50 Gene and Methods of Use Thereof
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APPLICANT: Abj. Kanako
APPLICANT: Matsuhisa, Akio
APPLICANT: Matsuhiton: PROBES FOR THE DIAGNOSIS OF INFECTIONS
TITLE OF INVENTION: CAUSED BY STREPTOCOCCUS PYOGENES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 35; DB 2; Length 1829; 56.5%; Pred. No. 0.85;
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; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: INTRON 1 OF RAD50 GENOMIC SEQUENCE
US-08-687-080-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY AGENT INFORMATION:
ANNUMBER AGENT INFORMATION:
                                                                                                                                                                                ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sholtz, Charles K.
REGISTATION NUMBER: 38.615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
Sequence 57, Application US/08687080 Patent No. 5965427 GENERAL INFORMATION:
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Patent No. 6245906
GENERAL INFORMATION:
APPLICANT: Ueyama, Hiroshi
APPLICANT: Abe, Kanako
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pairs
                                                                         APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human R2
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
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Best Local Similarity 56.58
Matches 65; Conservative
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MEDIUM TYPE: Floppy of
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STRANDEDNESS: double
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ZIP: 94306
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STATE:
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> RESULT 7 US-08-687-080-57/c

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 2-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10930
FRIDR APPLICATION NUMBER: PCT/US92/10930
FRIDR APPLICATION NUMBER: US 08/327,392
FRIDR APPLICATION NUMBER: US 08/327,392
FRIDR APPLICATION NUMBER: US 08/327,392
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US 08/62,443
FILING DATE: 11-OCT-1994
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,839
FILING DATE: 11-DEC-1991
APPLICATION NUMBER: US 07/805,093
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
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APPLICATION NUMBER: US 07/805,093
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APPLICATION NUMBER: US 07/805,093
FRIDR APPLICATION NUMBER: US 07/805,093
FRIDR APPLICATION NUMBER: US 07/805,093
FRIDR APPLICATION NUMBER: 33,229
                                                                                                                                                                         APPLICATION NUMBER: US/08/545,860D FILING DATE: 07-MAR-1996
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAR (215) 568-3439
INFORMATION FOR SEQ ID NO: 63;
SEQUENCE CHARACTERISTICS:
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8304..8342
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2353..2484
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6788..6934
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7967..8062
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595..666
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL: N
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LOCATION:
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FEATURE:
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; LOCATION:
US-08-545-860D-63
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FEATURE:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/381,862
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1997-71077
FILING DATE: 25-MAR-1997
FILING DATE: 25-MAR-1997
PRIOR APPLICATION NUMBER: PCT/JP98/01288
FILING DATE: 23-MAR-1998
ATTORNEY AGENT INFORMATION:
NAME: CAWLEY, Jr., Thomas A.
REGISTRATION NUMBER: 40,944
REPRENCE/DOCKET NUMBER: 19036/36274
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-648
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2546 CAAAAGACGGTCTGACTTATACTTATACTCT 2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 cctcggacggactcacttatacttttaaact 396
                                                                  Illinois
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Streptococcus pyogenes
; STRAIN: Clinical Isolate SP-6-28
US-09-381-862-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3549 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linea
MOLECULE TYPE: DN
ORIGINAL SOURCE:
                             Chicago
                                                                                                                       90909
                                                                                             COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Chaganti, Raju S.K.
APPLICANT: Dyonin, Vadim
APPLICANT: Dyonin, Vadim
TITLE OF INVENTION: CLONING AND USES OF BCL-8
FILE REFERENCE: 53828-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/450,852
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1728 agaactgaatcttatactaaactgggtgcctt 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2030 tgacattagatattttctatattgtctgcatt 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09450852
Patent No. 6309860
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.1
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Best Local Similarity 60.99
Matches 56; Conservative
          CDS
3032..3145
                                                            CDS
6788..6934
                                                                                                                 CDS
7967..8062
                                                                                                                                                                  CDS
8304..8342
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US-09-450-852-3
                                                                                                               NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
PCT-US94-04496-63
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US-08-617-860B-3/c
                                                                            LOCATION:
FEATURE:
                                          FEATURE:
NAME/KEY:
          NAME/KEY:
LOCATION:
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SEQ ID NO 3
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PCT-US94-04496-63/C
Sequence 63. Application PC/TUS9404496
Sequence 63. Application PC/TUS9404496
Seneral INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Croanani, Elsonostics, Therapeutics and Methods
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                              182 TGTACTTCCTGGGGTACAAAGAAGCAGGATGCCTTACCTCTACATGCCCACTACTGGCAC 3123
                                                                           3302 CCTTCCTAAAATCTCTAAAATACTTCAAAAACATTTCTTTAGCTGGTTAAACAGGGAATA 3243
                                                     658 cgttcataaatctcaaagaaccctgcaatccaaatctctacctatagcaagcggagcttt 717
                                                                                                                      718 ctatcctaaaaatatcaaaacaaaaaacaatggataaaactctcaaaaaaccctcactacta 777
                                                                                                                                                                                          778 taatcaaagtcaggtggaaactaaaacgattacgattcacttcattcccgatgcaaacac 837
                         0; Gaps
                     92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: Norris STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US94/04496
Best Local Similarity 49.5%; Pred. No. 2.3;
Matches 90; Conservative 0; Mismatches
                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TJU-1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: DeLLOE ESQ., MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUT-
TELECOMMUNICATION INFORMATION:
TELEPRONE: (215) 568-3100
IPELEFAX: (215) 568-310
INFORMATION FOR SEQ ID NO: 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8342 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 8342 base pai.
TYPE: nucleic acid
STRANDEDNESS: single
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2353..2484
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595..666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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ZIP: 19103
                                                                                                                                                                                                                                                                                                 3122 AG 3121
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
FEATURE:
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                                                                                                                                                       718 ctatcctaaaaatatcaaacaaaaacaatggataaaactctcaaaaaaccttcactacta 777
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                                              Gaps
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1.9%; Score 34.8; DB 5; Length 8342; 49.5%; Pred. No. 2.3; Live 0; Mismatches 92; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.9%; Score 34.4; DB 4; Length 2340; 60.9%; Pred. No. 1.5;
Live 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/08617860B
; Patent No. 6133506
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STRAIN:
                                                 STREET:
                                                                     STREET:
                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131 aacatcaaaaaacaagagatggcacaacgccaagcttacgctaaaaaactctttaaagaag 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                APPLICANT: Tvpfer, R., Bautor, J., Bothmann, H., Filsak, E., APPLICANT: Hvricke-Grandpierre, C., Klein, B., Martini, N., APPLICANT: M. Iler, A., Schulte, W., Voetz, M., Walek, J., APPLICANT: Schell, J.
TILLE OF INVENTION: Promoters
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33.2; DB 3; Length 3350; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1191 ctttagaagaactccaaatcactgctaaagatctcgaacatcttaatctt 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1939 AAATAAACTAACAAATCACTTCAACTAATTTTGGTTCTCTACCAT 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Indels
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,860B
FILING DATE: 01-MAR-1996
PROR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGGUS BIOPLASTIC
                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                       E: Steinberg, Raskin & Davidson, P.C. 1140 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(2611..2908, 3001..3341)
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/EP94/02950 FILING DATE: 05-SEP-1994 APPLICATION NUMBER: DE P4329951.2 FILING DATE: 04-SEP-1993 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3350 Base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic Lambda FIX II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/08241943; Patent No. 5602321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%;
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Conservative
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2611..2613
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
                                                                                                                                                                                            New York
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                   10036
                                                                                                                                                       ADDRESSEE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-617-860B-3
                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY:
                                                                                                                                                                           STREET:
                                                                                                                                                                                            CITY: STATE:
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627 taaaacttttagctcttccagtcttttccccgttcataaatctcaaagaaccctgcaat 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 32.8; DB 1;
53.0%; Pred. No. 1.5;
ative 0; Mismatches 62;
Nicholas J. Seay, Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Nicholas J. Seay, Quarles & Brady
                  First Wisconsin Pláza, One South
Pinckney St.,
P.O. Box 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-229-9076-8
                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: us/07/980,521
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/241,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Gossyplum barbadense
Sea Island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08378588 Patent No. 5608148
                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Seay Nicholas J. REGISTRATION NUMBER: 27,386 REFERENCE/POCKET NUMBER: 11. TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 251-2484
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APPLICANT: John, Maliyakal E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 70; Conservative
                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
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                                                                                                              COUNTRY: USA
ZIP: 53701-2113
                                                                          Madison
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ORIGINAL SOURCE:
ORGANISM: GOSS
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LIBRARY: EMBL-
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US-08-241-943-5
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US-08-378-588-5/c
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Patent No. 5869720
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE
CORRESPONDENCE ADDRESS:
                                                                                                                COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PREDICTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,588
                                                                                                                                                                                                               APPLICATION:
FILING DATE:
CLASSIFICATION:
ROASSIFICATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-29-9101-2
FELEPHONE: 6608 251-2484
FELEPHONE: (608) 251-2484
FELEPHONE: (608) 251-2166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOWNED: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nicholas J. Seay, Quarles & Brady STREET: First Wisconsin Plaza, One South STREET: Pinckney St., STREET: P.O. Box 2113
First Wisconsin Plaza, One South Pinckney St., P.O. Box 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Gossypium barbadense
STRAIN: Sea Island
IMMEDIATE SOURCE:
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Best Local Similarity 53.0%
Matches 70; Conservative
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                                                                                 COUNTRY: USA
ZIP: 53701-2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: GOSS;
                                                    Madison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LIBRARY: EME
; CLONE: SIB8
US-08-378-588-5
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US-08-811-094-5/C
                                                                     STATE:
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627 taaaaacttttagetetteeagtettttteeegtteataaateteaaagaaeeetgeaat 686
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CLASSIFCATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,588
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 27,386
SEQUENCE (608) 251-2484
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: Gouble
CONFIGURATION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF T
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Job time: 2316 sec
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STRAIN: Sea Island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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; LIBRARY: EMBL-SI
; CLONE: SIB8
US-08-811-094-5
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| 18 | RESULT 1 CNSOOLOO 1101 bp DNA linear GSS 03-JUN-1999 DEFINITION DASOPHila melanogaster genome survey sequence TET3 end of BAC: BACR32D23 of RPCI-98 library from Drosophila melanogaster (fruit ALO68607.1 GI:4958689 ALO68607.1 GI:4958689 ALO68607.1 GI:4958689 ALO68007.1 GI:4958689 ALOSOPHIA melanogaster CNEWRDS GSS. SOURCE ORGANISM Drosophila melanogaster ENEATYORIS HOSOPHIA: Ephydroidea: Drosophila in Neoptera: Endopterygota: Diptera: Brachycera; MUSCOMORPIA: Ephydroidea: Drosophiliae; Drosophila. REFERENCE 1 (bases 1 to 1101) AUTHORS GENOSCOPE. TITLE Direct Submitseion SUBMITTED (02-JUN-1999) GENOSCOPE - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr - Web: www.genoscope.cns.fr - Web: www.genoscope.cns.fr) COMMENT COLABORATION with the Berkeley Drosophila Genome Profect (BAGP). | The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Arron Mammoser in Pieter de Jong's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EGY libraries. A more detailed description of the library and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library and how to order individual Ency Cones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm. Commonweight |---|--|---|
| GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: July 26, 2002, 02:57:07; Search time 1946.51 Seconds (without alignments) 12474.132 Million cell updates/sec. Title: US-09-824-567-1 Perfect score: 1799 Sequence: 1799 Scoring table: IDENTITY_NUC Gapext 1.0 Searched: 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: 27472414 Minimum DB seq length: 0 Maximum Match 08 Maximum Match 1008 Listing first 45 summaries | Database: Database: EST:* 1: em_estba:* 3: em_estin:* 4: em_estin:* 5: em_estin:* 6: em_estpo:* 7: em_estro:* 8: em_estpo:* 10: gb_est:* 11: gb_hc:* 12: gb_gss.* 13: em_gss.hu:* 14: em_gss.hu:* 15: em_gss.hu:* 16: em_gss.lu:* 16: em_gss.lu:* 17: em_gss.lu:* 18: em_gss.lu:* 18: em_gss.lu:* 19: em_gss.lu:* 10: gb_hc:* 10: gb_hc:* 11: gb_hc:* 12: gb_hc:* 13: em_gss.lu:* 14: em_gss.lu:* 15: em_gss.lu:* 16: em_gss.lu:* 18: em_gss.lu:* 19: em_gss.lu:* 10: em_gss.lu:* | 53.4 3.0 1101 12 CNSO0LOO |

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         557 МСМИТСТАТСИНСИТСИНМАУСМУССМСҮТТСМССМАННІМАМАСАМІМАНАСНІНІНИ 616
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                                                   489 others
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                                                                                                                                                                                                                                                 107; Conservative 224; Mismatches 265;
                                                                                                                                                                                           Score 53.4; DB 12;
Pred. No. 0.084;
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                              /note="end : TET3"
166 c 7 q
/clone="BACR32D23"
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CNS017HL 1101 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
                                                                                                                                                                                                                                            isogenic strain y2; cn bw sp, the same strain used for the BGCP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                      please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1098 МИННТТИММИМСМНТААМИМАМИМИМИМИМАМАМАМИМСИМСМСМСМСНИМСААМИМ 1039
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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/db_xref="taxon:7227"
/db="psc:98"
/clone="BACR48P19"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR25K05 of RPCI-98 library from Drosophila melanogaster (fruit AL059199
                                                                                                                                                                                                                           web: www.genoscope.ons.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDDP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DRA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
BACN17H08 of DrosBaC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Mismatches 154; Indels
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Pred. No. 0.45;
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/clone="BACN17H08"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRi dispession of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Conservative 137; Mismatches 194;
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21.9%; Pred. No. 1;
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/clone="BACR25K05"
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/clone_lib="RPCI-98"
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"Web: www.genoscope.cns.france (E-Mail: Sequelegenoscope.cns.rr

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Location/Qualifiers

Inne
       CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACROSKIO of RPCI-98 library from Drosophila melanogaster (fruit
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Conservative 251; Mismatches 215;
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1101 bp
                                                            fly), genomic survey sequence.
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                                                                                                           AL063921.1 GI:4941778
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila denome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Razutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the Isogenic Strain y2; on bw sp, the same strain used for the BDGP's PI and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://pacpac.med.buffalo.edu/drosophila_bac.htm.
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939 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACKZ6H16 of RPCI-98 library from Drosophila melanogaster (fruit
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                     1034 АТИМИМИМИТАТАМИАСТСННИТИУНГНСТИХУННТУНМИМАМИМАМИМИНИКАНҮНИАН 1093
                                                                                                                                                                                   974 YCCHYYCTCHTHATTHYHYMCTCYHYCTWHTYWTAYWWAWTAHAMTTATWWWWMHWWAHW 1033
631 acttttagetetteeagtetttteeegtteataaateteaaagaaeeetgeaateeaa 690
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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/db_xref="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGF) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC dibrary (Dros BAC) was made by Alain Billand at CEPH (Centre disturbed out Polymorphisme Humain) with funding provided by a MRC project grant. The DRA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                             GSS 26-JUL-1999
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                          Drosophila melanogaster genome survey sequence SP6 end of BAC BACN03G04 of DrosBAC library from Drosophila melanogaster (fruit AL098379
                     457 MAMANAMAYAMAMAMAMAMAMAMAMAMAHAMAMAHHYMAMAMAHMAMAMHHATHHAMAM 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101 МИВИУТИКИНИКИТАКИТАНБИУНКИАТМИМИКНТНЯННЕНТНИКНТИТИТАТТНЯ 1042
728 aatatcaaacaaaaacaatggataaaactctcaaaaaaccctcactactataatcaaagt 787
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                                                                         838
                                                                                                  Length 1101;
                                                                  788 caggiggaaaciaaaacgaitacgaitcacticaitcccgaigcaaacaca
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN03G04"
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Matches 117;
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16D23 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                          994 attcccctcaacaatatgaagcttagagaagccttagcatcagccttagataaggaagc 1053
                                                                                                                                                                                                                                                                                                                                                                                                               tottgtotoaactatattottaggccgtgcaaaaactgccgatcatctcctacctacaaa 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1114 tattcatagctatcccgaacatcaaaaacaagagatggcacaacgccaagcttacgctaa 1173
                                               801 АННҮНҮСТМИНМЕТНИИСНИНСНҮМТМНННҮНТМҮТААММАААААААААААА 742
                                                                                                                                                     741 AAAM-------MAAAMATWIAIMITAITIATHIIIYAIMIYWIWHYHCMIMS 696
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814 tcacttcattcccgatgcaaacacagcagcaaaactatttaatcagggaaaactcaattg 873
                                                                                                                                                                                                                                                                                                                                                                                                                                            575 YHTYTCHAYHTWHCWCWAHAMYKCYHAMMACAYANAMAHAMAYWMYIWAMHHHHAWWC 516
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Pergyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

    (bases 1 to 1101)

                                                                                                  874 gcaaggacctccttggggagaacgcattcctcaagaaaccctatccaatttacagtctaa
                                                                                                                                                                                                                                                                                                                                                       635 WCYMYCIMAHTHMWHWHWWHTHAHHAAHTWAAACWCHAMATHAHTMCHTHMHMTNTT
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1 Similarity 21.4%; Pred. No. 5;
82; Conservative 128; Mismatches 173; Indels
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/plasmid="pBeloBAC11"
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/note="end : T7"
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Drosophila melanogaster
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Direct Submission
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Submitted (13-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fx)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.depp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNS0168G 1201 bp DNA linear GSS 26-JUL-19
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15114 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                         611 ccaacctcgcatttcttaaaaacttttagctcttccagtctttttccccgttcataaatct 670
                                                                                                                                                                                                                                                                                                                                     671 caaagaaccctgcaatccaaatctctacctatagcaagcggagctttctatcctaaaaat 730
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656 HAAAXYHCYAAAHYYYYYYYYYYYYYYHWHYHYYHYYYYYYHAYYY 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 atcaaacaaaaacaatggataaaactctcaaaaaaccctcactactataatcaaagtcag 790
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                                                                                                                                                                                                                                                                     596 CWHANCICYCWCYAYMTMAAACCYAIMCCACYACYYYCCYCYMYYCYYYYTYAAYTAYYA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791 giggaaactaaaacgattacgattcacttcattcccgatgcaaacacagcagcaaacta 850
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
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                                                                                                                                         54; Conservative 104; Mismatches 104;
                                                                                DB 12;
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20.6%; Pred. No. 6;
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/db_xref="taxon:7227"
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/clone="BACN15114"
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                                                                                                           Similarity
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP 191 JULYON DATA CONTROLL OF THE STATE OF A PART OF A CALLABOTATION Of THIS BAC-end sequence was carried out as part of a Collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila Constructing a physical map of the Drosophila Constructing a physical map of the Drosophila Constructing a physical map of the Drosophila Constructing a physical map of the Drosophila Construction when the Drosophila Construction was a part of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the Drosophila Construction of the 
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DIOSOPHIA melanogaster genome survey sequence TET3 end of BAC #
BACR11F03 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 ctcaggaatctatgcttttgccttgaatccaattaaaaatgtacgaaagatccaagaggg 540
                                                                                                                                      900
                                                                                                                                                                                     760 BCBCAAAAMAAAAAMYCTMAYYBYBAWTYAAAAAAYAAYYYYYYYCWBHYYYYAYAWW 819
                                                                                                                                                                                                                                                        601 cctggaatccccaacctcgcatttcttaaaacttttagctcttccagtctttttccccgt 660
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                                                         700 YYYAYYYYYYYYYYYYYYYCWYYYCAATYYCYYYYAAMAANBCYYAAABCMTCABAAAA 759
                                                                                                                                                                                                                                                                                                                       820 AAHCAAAHCTCTAAAAAAAAAAYYYYYAAAYYCTYCACAAWYYYCCAAYCYYCAYYYYCC 879
                                                                                                                                                                                                                                                                                                                                                                                       tcataaatctcaaagaaccctgcaatccaaatctctacctatagcaagcggagctttcta 720
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Drosophila melanogaster
Eukaryota: Metazoa: Arthropoda: Tracheata; Hexapoda: Insecta;
Pterygota: Neoptera: Endopterygota; Diptera: Brachycera;
Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.
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WHEN : WWW.GENDSCOPE.CHS.FT)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.ffuitfily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://pacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR01J16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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1674 acttecgttatgetaaggaaaattageacetettttaatetegeaaaettgteaagaaet 1733
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Pterygota: Neoptera: Endopterygota; Diptera: Brachyeera;
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AL Chustes, L.C. 1999) Genoscope - Centre National de Sequencage :
By 1919 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Web : www.genoscope.cns.fr)

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Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Suspension cultures of L.esculentum E6203 were grown in Murashige and Skoog based medium, supplemented with 15% cocount milk (filter sterilized and added after autoclaving), 2% saccharose, and Img/ml 2,4D (pH5.8). Fresh medium was added every 7 days, and cultures were sprown art 25 C, with 12hrs of light and continuous
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                                                                                                                                                                                                                                                                                      314 TWITITITITITITINANNIWIWITAINNIANINITAITITAAAMAAACAAMAACACCMAAWA 373
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
                                                                           Length 555;
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1 (bases 1 to 570)
van der Hoeven,R., Sun,H., Bezzerides,J., Cho,J., CRoning,C. and Tanksley,S.
Generation of BSTs from Tomato Suspension Cultures Unpublished (2001)
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/lab_host="SOLR"
                                                                    2.4%; Score 43.8; DB 12;
illarity 39.4%; Pred. No. 12;
Conservative 26; Mismatches 157;
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/db_xref="taxon:4081"
/clone="cTOS21020"
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                                                                                           Similarity
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Best Local Simi
Matches 119;
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Tetraodon nigroviridis genome survey sequence T7 end of clone
124ED6 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large
scale clone-nd sequencing project of the Terraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Barnot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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Tetraodon nigroviridis DNA sequence
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/db_xref="taxon:99883"
/clone="112460"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG124BC03LP1-end : T7"
1 113 c 31 g 145 t 68 others
                                                                                                 1081 ТАММИМНИМАМНИТМТИМНАНТНАТНИАМАММИТМНИТМИНИТМНИТМНИММИМТ 1022
                                                                                                                                              574 tectaatgaatetacaettgttgttaeeetggaateeeeaaeetegeatttettaaaaet 633
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1 (bases 1 to 555)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fis Bouneau, L., Bllault, A., Quetier, F., Saurin, W., Bernot, A. Weissenbach, J.
                          Indels
  ed. No. 10;
Mismatches 144;
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    Pred. No.
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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Similarity 16.8%; Pre 57; Conservative 139;
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Direct Submission
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Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila demome project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitily.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; on bw sp, the same strain used for the BDGP's
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence TET3 end of BAC # BACH14D09 of RPCI-98 library from Drosophila melanogaster (fruit Ily), genomic survey sequence.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                659 gitcaiaaaictcaaagaaccetgeaaiccaaaicteacciatageaageggagetite 718
                                                                                                                                                                                                                                                                                                                                                                           719 tatcctaaaaatatcaaacaaaaaaaagataaaactctcaaaaaacccctcactactat 778
                                                                                                                                                                                       599 accetggaatececaacetegeatttettaaaacttttagetetteeagtettttteeee 658
                                                                                                                                                                                                                                 145 AACCIGGIACTCCTAAACAIACATITCCTCAAACAICITIACCACCICTIACACCICCIC 204
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 922)
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Location/Qualifiers
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                                                                                                DB 10; Length 570;
                                                                                                                                               Indels
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                                                             Score 43.8;
Pred. No. 12
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/note="end : TET3"
. 95 c 109 g
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Drosophila melanogaster
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51.8%;
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Query Match Best Local Similarity

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GenCore version 4.5
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1 (sites)
Murdin,A.D., Oomen,R.P., Wang,J. and Dunn,P.
Murdin,A.D., oomen,R.P., Wang,J. and Dunn,P.
Chlamydia antigens and corresponding dna fragments and uses thereof
Patent: Wo 0174863-A 1 11-OCT-2001;
Aventis Pasteur Limited (CA)
                                                                                                                     AF305387 Bacillus
AE007859 Clostridi
AF000139 Borrelia
AF043071 Borrelia
AJ250012 Borrelia
AJ250013 Borrelia
AL003355 Agrobacte
AE008258 Agrobacte
M57689 Bacillus su
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Z99110 Bacillus su
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/codon_start=1
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BCT 01-DEC-2000

DNA linear BCT 01-DEC 103 of the complete genome.

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SOURCE

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Direct Submission
Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA Location, Qualifiers
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Olinger.L., Grimwood,J., Davis,R.W. and Stephens,R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
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1 (bases 1 to 11648)
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/gene="oppA_1"
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ATVAISGGKKIDFLAMRTTEILFSLPRIPIIILLJVIFHHGLLPLILAMTITGWIPIS
RIIYGOFLLLKNKPFVLSAKAMHASTFHILKKHLLPNTLAPIISTLIFTIPNALYTEA
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TPSMRIGMQIIETLRQHHKMNKEEAYNKAMQLLTDVCIPNPKYSFSQYPFELSGGMRQ
                                                                                                                                                                                     RVVIAIALASQPKLILADEPTTALDSWSOAQVLRILRNIOOOKOATILLYTHNISLVK
BLCNDICIIKDGKLIETGTVEBIFLSPKHPYTLKLINAVSKIPIKKTSSPILKNKFQP
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/product="Oligopeptide Transport ATPase"
/protein_id="AAb18355.1"
/db_xref="G1:4376473"
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/transl_table=11
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/gene="oppF"
/note="CPn0202"
10578. .11366
/gene="oppF"
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/note="CPn0201"
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/gene="oppD"
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1373 CGACCCCTTAACAGCTGAAGACTTTATAGAATCTTGGAAACAAGTAGCTACTCAAGAAGT
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PSGYPPYAINHKGFLEILGNIEGEODHOKRSELVSGASLYLETFHIIBPIYHDAFQFA
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LDQGLKDEILGTLAGDDTIFVTPIDEGRLPLLMVSIANLLQVFLD"
3263. 3916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MLTLGLESSCDETACAIVNEDKQILANIIASQDIHASYGGVVPE
LASRAHLHIFPQVINKALQQANLLIEDMDLIAVTQTPGLIGSLSVGVHFGKGIAIGAK
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INEYFRSAIQTACNLPVYFPPAKLCSDNAAMIAGLGGENFQKNSSIPEIRICARYQWE
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PSKITKILANSYYVTVTRGTPLFTQILIITYFQLPEULPEPPPLWGIJALSMNSAAYL
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ILMVVGVPELTKVTKDIVSRELNPMEMYLICAGLYFMATTSRSCISRLSFRKRSYDN
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KAFELLHLLDIERSVAKNYPDQLSGGGKQRALVRSLCMDKHTLLFDEPTSALDFFATA
SFRHLLETLRDQELTVGLTTHDMQFVHSCLDRIYLIOGGTVAGVYDKROBELDSGHPL
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/protein_id="AAF38394.1"
/db_xref="GI:7189488"
                                                                                                                                                                                                                                                                         /note="O-sialoglycoprotein endopeptidase; identified by match to PFAM protein family HMM PF00814"
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/protein_id="AAF38393.1"
/db_xref="G1:7189487"
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/gene="CP0575"
/note="similar to SP:P10345 PID:41572 GB:U00096
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                                                                                                                                                                                                                                                                                                                                                                                            /product="O-sialoglycoprotein endopeptidase"
/protein_id="AAF73688.1"
/db_xref="GI:8163461"
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/product="arginine repressor"
                                                                                                                                                 complement(1653. .2687)
/gene="CP0573"
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/gene="CP0577"
complement(4620. .5978)
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/db_xref="GI:7189486"
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/transl_table=11
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/gene="CP0574"
2771. .3214
/gene="CP0574"
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3263. .3916
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/gene="CP0576"
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/gene="CP0576"
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1. .11764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydophila pneumoniae AR39.
Chlamydophila pneumoniae AR39
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 11/54)
Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Elsen,J. and Fraser,C.M.
Genome sequences of Chlamydia trachomatis MoFn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., Direct Submission
                                                       2513 TICTCTTTACCTAGAGACCTTTCATATTGAGCCGATCTACCAGGACGCATTTCAATT 2572
                                                                                                                                              1621 tgctatgaataaaaaactttctaatctaggagtctcaccaacaggagttgtgggacttccg 1680
                                                                                                                                                                                2573 TGCTATGAATAAAAACTTTCTAATCTAGGAGTCTCACCAACAGGAGTTGTGGACTTCCG 2632
                                                                                                                                                                                                                                                                   1681 ttatgctaaggaaaattagcacctctttaatctcgcaaacttgtcaagaactgaatctt 1740
                                                                                                                                                                                                                                                                                               2633 TTATGCTAAGGAAATTAGCACCTCTTTAATCTCGCAAACTTGTCAAGAACTGATGATCTT 2692
                                                                                                                                                                                                                                                                                                                                                                                  2693 AIACTAAACTGGGTGCCTTTGTGGCGCTCGTTTCCTTCTGACTGCTCTTCTCTCT 2751
                           ttetetttaeetagagaeettteatattattgageegatetaeeaegaegeattteaatt
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complement(109. .1707)
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/db_xref="taxon:115711"
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complement(109. 1707)
/gene="CP0572"
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YRVJGLGEPKNGEDAVSKDYLERYVSSQLTIDKVEDKPITKPNIGKLLYSQGTSPKLE
GPLEJLGLIJSGIGGTHWSASKSNOSSFPSALRHKETESDTDCPQITSTLSGNOAG
TYTWSLSLKVLYPSIFQLERPVQLSLYSYEDMILPIDNIFNMSOPRITFLALLGGTM
LAGGKYDILLELAAHQTNOTLMISPNCSRFSILQLKOTVNOFENSPVDFYIVHAAHSCHWS
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FRLQQAQLEHTYLAR IFPQPFVINVPLDVAYYSLNIEGTYKNAHLEADAILDNPLKL
SCSMGGARKNELFRQGTYFFNKKWQELLSPHFSYRARRESCRAQITOTNIEFPRFSG
KITARRNELLIHARYGSSVBFYKFETTSILIHQGFCSLFLSLUSSHLAPFHLKKIFFS
FHTDGGKFVTKGNLQALIENPDYPDLNNTRIJIPDLLLSLDESSTSPSSKDLKIQGS
EIFSLPLDSITKTYGKQVRLSEYFGSSGDLNFVVNYNPRDQNKLTLISNFKSEALLGE
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QLVEESIEESLGQQDQLIQSVLIEISDKFLSSIGETLSGNLDMNQNVIQGLLIKENPE
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GLKAQISSLAGPRINVSIKNAFRFGEGPVDIMVDSENLQAQIPLILNEKSILLKENLT
AHLSINEDVNKAFLQERNPLLAGGAYSQYPVTLEIDKQNFYLPIRPYSFEFFRIQSAT
LDMGKISIANIGTMYALFQFLDITDQKQFVESWFTPIFFSVQKGSIIGKRXDALIDRR
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GFYLEKSSEKFWIKCVVSEDQQSGNIFIESVLSPDVSISAQFSSVPVAFFKIFIASPF
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IELKPELASALCNOIIPLSTPITSKQIHATVSYAKIPLDITKWKHIEITSQAQLPEVA
                                                                                                                                                                             translation="MRKRHSFDSTSTKKEAVSKAIQKIIKIMETTDPSLNVETPNAEI"
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SAYARIALLKSYSLGNPFSSLADKLFSSLGDSTPPPTVHPFPWEKSNFDSIENK"
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CVLSYYGLLTCVPILVFFLRLSGHLFTNLNWKEWLIIKFPDYKKPIVAIVEAAYHATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="conserved hypothetical protein; identified by
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99.98;
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| Nucleic Acic 20330349 2 (bases 1 Shirai,M Direct Submi Submitted (C School of Me Minamikogush | (E-mail:msni Fax:81-836-2 On Aug 31, 2 gi:6172288 g | gi:6172320 g gi:6635164 g gi:8547426 g AB033780-ABC | AB038345-AB0 AB036071-AB0 Loc 1. | /st /st /db | eb/ eb/ eoo | /co /tr /pr | /db /tr ATQ ATQ 573 | /ge 573 /ge /ge | /tr /pr /gb | /tr LAI 895 | 895 /ges /cox/ | /pr /pr /tri /tri /tri /rri /pr /pr /pr /pr |
|--|--|--|--|---|--|--|---------------------------------|---|---|---|--|--|
| JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL | COMMENT | | FEATURES Source | | gene | | gene | CDS | | dene | CDS | g gene CDS |
| | 11 acaagagatggcacaacgccaagcttacgctaaaaaactctttaaagaagctttagaaga 1200 | 01 actecaaateactgetaaagatetegaacatettaatettatett | 51 agcaagttettaetagteeaaettataegagaaeagtggaaagatagttagggttege 1320 | 21 tatcoctattgtcggaaaggaatttgctcttctccaagcagcctatcttcagggaactt 1380 | 1 ctctttagctacaggagatggttcgcagactttgctgatcctatggcatttctaacgat 1440 | otttgettatecateagaatteeteettatgeaateaaceataagaetteetagaat 1500 | | 1 ttctotttaoctagagacotttoatattattgagoogatotaooacgaogoatttoaatt 1620 | 1. tgctatgaataaaaactttctaatctaggagtctcaccaacaggagttgtggacttccg 1680 | 1 ttatgctaaggaaaattagcaccttttaatctcgcaaacttgtcaagaactgaatctt 1740 | 1 atactaaactgggtgcctttgtggcacctcgtttccttctgactgctttctctctc | AP002545 Chlamydophila pneumoniae J138 genomic DNA, complete sequence, section 1.4. N Section 1.4. AP0052545 AB033796 AB033791 AB033792 AB033793 AB033794 AB033795 AB033795 AB033795 AB033797 AB033797 AB033797 AB033797 AB033797 AB033797 AB033797 AB033797 AB0336073 AB033797 AB033607 AB03607 AB03607 AB03607 AB03607 AB03607 AB03607 AB03607 AB03607 |
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| 97 97 97 | QY Db | Qy Db | 0y Db | Qy Db | Oy Db | QQ Dp | 0 <u>y</u> | QQ Dp | Qy Db | QY Db | Qy Dp | REI VEI VEI C (|

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CKEDALEGAELIDKERSREPLGKLANY VIGELIAR VTGHEF HE EKAGGVGAF ISL
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2000 this sequence version replaced gi:6172286
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gi:8547430 gi:8978379; submitted (25-oct-1999)
B038381, Ab033792-Ab033799; submitted (25-oct-1999)
B038377; submitted (14-Feb-2000)
                                                                                                                                            (04-JUL-2000) Mutsunori Shirai, Yamaguchi University
Medicine, Department of Microbiology; 1-1-1
shi, Ube, Yamaguchi 755-8505, Japan
hirai@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oroduct="Glu-tRNA Gln amidotransferase (C subunit)"
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strain="J138"
ids Res. 28 (12), 2311-2314 (2000)
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gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 233705 ACTICCCCCCTGCIAAACIAIGCTCAGATAAIGCTGCTATGATTGCAGTCTAGGGGGAG 233764
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PAT 06-FEB-2002 ö 235384 1680 101 atgogcaagatatcagtgggaatctgtatcaccattctccttagcctctccgtagtcctc 160 281 gtcaaacatatctatgagggattagttcaagaaaataatctttcaggaaatatagagcct 340 Gaps ; Length 1599; chlamydophila pneumoniae. Chlamydophila pneumoniae Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila. linear 0; Indels /organism="Chlamydophila pneumoniae" /db_xref="taxon:83558" 1 389 c 261 g 440 t 1 (sites)
Ratti,G. and Grandi,G.
Immunisation against Chlamydia pneumoniae
Patent: WO 0202666-A 24 10.7AN-2002;
Chiron S.p.A. (IT) Query Match 88.9%; Score 1599; DB 6; Best Local Similarity 100.0%; Pred. No. 0; Matches 1599; Conservative 0; Mismatches 0; DNA Sequence 24 from Patent W00202606. AX349501 Location/Qualifiers 1. .1599 AX349501.1 GI:18615357 ۵ 509 RESULT 5 AX349501 LOCUS DEFINITION source ACCESSION VERSION KEYWORDS ORGANISM BASE COUNT ORIGIN TITLE REFERENCE AUTHORS 181 FEATURES SOURCE qq g ð Qγ δy δ g Qγ g ŏ g $\delta \lambda$ qq δŽ g ΩŸ

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                                    gaatctacacttgttgttaccctggaatccccaacctcgcatttcttaaaacttttagct
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PRIPSIIQGSKEVSLALFVLGTVLAIVGACAAAVGGAFSVCLGVLEGGTVLATGLLL
AVLEFCHIRSSMEKYVILTKQDLFKEPVIQEEQATPLIEEASYTCEPGIPLSGPEEVQ
QERPVILQKDLDLSHAPKIAVGSHVVELVKAGKIGRNGERLLEEGIDTDQNFVRWD
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VLDHSNIPLMFCNTYHLIVHPGAEAIAAMGGLHQFIGRNAPIITDSGGEPGIFSLAYGS
VAEEIKSCGKKKGGNTIIKVNDDGVHFKSYRDGRKLFLSPEISVQAQKDLGADIILPL
DELLPFHADPTYFHQSSQRTYVWEKRSLDYHLKNPGIQSWYGVIHGGFFPDQRKLGCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 11944)
Ralman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria: Chlamydiales: Chlamydiaceae; Chlamydia.

1 (bases 1 to 11944)
Stephens.R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R.,
Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q.,
Koonin,E.V. and Davis,R.W.
Genome sequence of an obligate intracellular pathogen of humans:
1501 TACCACGACGCATTTCAATTTGCTATGAATAAAAACTTTCTAATCTAGGAGTCTCACCA 1560
                                                                                                                                                                                                                     AE001293 11944 bp DNA linear BCT 30-OCT Chlamydia trachomatis section 20 of 87 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stephens.R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R.,
Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q.,
Koonin,E.V. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-MaY-1998) Program in Infectious Diseases, U of California, 235 Warren Hall, Berkeley, CA 94720-7360, Location/Qualifiers
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/protein_id="AAC67785.1"
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                                                                       /organism="Chlamydia trachomatis"
/strain="D/UW-3/CX"
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/protein.id="AAC67784.1"
/db_xref="GI:3328598"
                                              1661 acaggagttgtggacttccgttatgctaaggaaaattag
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Science 282 (5389), 754-759 (1998)
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/gene="tgt"
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complement(105..878)
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/codon_start=1
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VERSION
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FVEDLPFDGSAIGGSLGKNLODIVEVYGVTAANLSAERPRHLLGIGDLPSIWATVGFG
IDSFDSSYPTKAARHGMILTSQGPLKINNQRYSSDINPIEPGGSCLACSQGITRAYLR
HLERVHEPNAGIWASIHNMHHWQKVMREIREGILNDRI"
                                                                                                                                                                                                                                                                                                                                                           AYAVSCLPSDSRSTLYRNLDSTASKTAFTINTDSASRWAJFRNLSDGEICALIEGMPP
DEAIWVLDDIPDRRYRRILDLIDVKKALKIRDLQKHGRNYAGRLATNEFFRALITV
KEVATCIRNNPGIDLTRLVFVLDFKGELQGFVTDRSLITASPEMPLKQIMRPIEHKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADTTREEVULVERKKVALLPVVDEERRLIGAITYEDVVETIEDIADETIARMAGTTE
DVGYNDLVVORFLIRAPWLLITLCAGLVSASVMAYFQKIAPTLLAMVIFFIPLVNGL
SGNVGVQCSTILVRSMATGTLSFGRREFILKEMSIGLLFGVALGILCGLVVCCMGCL
GLGLFATGGVQLGVTVSVGILGASLTATTLGVLSPFFFAXIGVDPALASGPIVTALND
COMPLEMENT (4001. .5092)
                                                                                                                                                                                                                                                                                                                                     /translation="MDSKTSHLDDELCFKLEEAFDTLTAGEHSQDLTSIVSVYNPIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LERTAGKUDVLYGKKIOPFISROWERVILCEKEGEFIRPTOEPDWYMDVSLLDRTGSG
TAPVYTYPPMDAETVICWTSILLPTFSIVMLYNIFRFFIVPFYILFOMVRQNYQTD
IPKEFFYCSDIVEMTRSLLQAVKAPFYGAVCYLANLYGILNPLSGRVVLASIERDW
NNDYTRSRGVWGTECEKNYMFEGGGTRSGLGDNAWYLLGCFOPVQLFLKNDGVISGR
RPSIQSFPESKEYLASFLYGAVPGRLAGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MVSMSLNLPPAEVRLRPVTARSFPNSSAWRATQKRITGCSLNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYRPSSARVISEVVGVLVVLGWICFRIAYLANSRVLTFPKMFAIALLPFILFGGGLAI
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ILLGALILTGVITTIPSIAASYFLSLGVTLVIVGAGLCAAFKRPLFSVTQSKASTLLH
$50.0"
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GETFDKVARFLGLPYPGGGKLEELAREGDADAFARSPARVSGYDFSFSGLKTAYLYAL
KGNNSSARAPPPRYSETGKRNIAASFQKAVFWTIAQKLPDIVKTFSCESLLYGGGGVAN
NSYFRRLLNQICSLPIYFPSSQLCSDNAAMIAGLGERLFCNRTHYSKEVIPCARYQWE
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ASRAHLQTFPELLTAATQSAGVSLEDIELISVANTPGLIGALSIGVNFAKGLASGLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="O-Sialoglycoprotein Endopeptidase"
                                                                                                                                                                                                                                                              /product="Mg++ Transporter (CBS Domain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAC67787.1"
/db_xref="G1:3328601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
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/db_xref="G1:3328602"
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/db_xref="G1:3328600"
                                                                                                                                                      complement(2150. .3562)
/gene="mgtE"
                                                                            complement(2150. .3562)
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/transl_table=11
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/transl_table=11
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/transl_table=11
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/note="CT198"
6692. ROYE
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/codon_start=1
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5316, FF?
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/codon_start=1
                                                                                                                                /note="CT194"
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/note="CT197"
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                                                                                                       /gene="mgtE
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YKOOBAITLAKSLLEBALTELÄNTIEDLEKYPLTESATSYMNSQIAQMLRDQWRRSLG
ITFPICGKEYALLQNDLIGNTFFMSIGGWFADFSDPLAFLSIFSKGVKRYALODPOF
DQLILSIETEKNPQKRSALISBASLYIERQNVIEPLYHDVFHYTTNNKLSFVRLHPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLSYIKRRLLENLLSLWVVVTLFFIIKTIFCDPFNDENGNILS
SETLALKRNRYGLÖKPLETQYLIYLKCLLTLDFGESLIYKDRTVISIIAAALPSSAIL
GLESLCISLFGGITLGILAAFYKRSCGRTIFFSSYIQISYDAFYIGAFDLQYFAIKYS
CLPIACWGRRFHTLDFSIALATTPMAFITQLTCASVSANLKKDVYLLAYAKGLSPFKV
LIKHILPYALFPVISYSAFLITTLMTOTFSIENLFCIFGGKWFICSIKQFRDYFTLC
LSVFKGAFFMITSLCCDLLQAMIDPQIRYSYGKERSK"
                                                                  /translation="MRKISVGICLLLALATSGCSKSSSNATHRSPATHTVAVSVKDDP
                                                                                                                                                                                               SGTSWLTFNTAKKPFSHSKLRQALSLVLNKEALASLAFVKPAKHLLPAHLHTYPEQPS
                                                                                            RTFDPREVRLLSDINLIHHLYEGLVQETPSGEVFPALAESFFLSEDKKTYTFNLKKAF
WSNGDLITAHDFVRSWNDVLQNRVASIYSFAFLPIDVNKDSGFFRKDDHTLVINLLTP
                                                                                                                                               TPHFLKLLTLPVFYPVHSQHQIRKEEKSLPISTGAFFLKEKKDRRWLKLEKSPYYYNK
                                                                                                                                                                         DQVAVQEICIHIIPDQQTASALFNQGKLDWQGLPWGHSIPQETLATTNKRRAPRSFDI
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YQQFLLLENKEFVLSARALQASTFHILRKHLLPNSLGPIISTLIFTIPNAVYTBAFIS
FLGLGIQPPYASLGTLVKEGIHSLAYHPWLFFIPSFFMIIVSVSFNCIGEGLRTKLLE
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TPSNRVGAQIVETLRHHFDMSKEEAFSKARELLESVHIESPDRCLQLYPFELSGGMCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 acttccccctgctaaactatgctcagataatgctgctatgattgcaggtctagggggag 60
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                                                                                                                                                                                                                                                                                                      LVDMRYAKNS"
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Best Local S
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| Db 7687 GCCTTCTTATAAGCAACAAGAGGCCATCAC | 1195 | Db 7747 GACTGAGCTTAACATGACTATTGAGGATCT | | Qy 1315 gttcgctatccctattgtcggaaaggaatt1 | Qy 1375 gaacttctctttagctacaggaggatggttc Db 7927 TACTTTATGTCTATAGGTGGGTGTTT | Qy 1435 aacgatctttgcttatccatcaggagttcct 1 1 1 1 1 1 1 1 1 | Qy 1495 agaaattctacaaaacatagaacaagagcaa | Qy 1555 gcaagcttctctttacctagagaccttcat | Qy 1615 tcaatttgctatgaataaaaactttctaat | Qy 1675 cttccgttatgctaaggaaaattagcacctc | RESULT 7 AE002215/c LOCUS AE002215 12980 | NOITI SION ON | _ | REFERENCE 1 (bases 1 to 12980) AUTHORS Read, T.D., Brunham, R.C., Shen White, O., Halkey, E.K., Peters' Rase 5 libber & Repriv R. Rase 5 libber & | Bowman, C., Dodson, R., Gwinn, M MCClarty, G., Salzberg, S.L., E Genome sequences of Chlamydia pneumoniae AR3 | | AUTHORS Read, T.D., Brunham, R.C., Shen, White, O., Hickey, E.K., Peterse Berry, K., Bass, S., Linher, K., Rowman, C., Dodson P. Godina B. | McClarty, G., Salzberg, S.L., E. TITLE Direct Submission JOURNAL Submitted (OI-MAR-2000) The II | COMMENT On Jun 1, 2000 this sequence FEATURES Location/Qualifiers source 112980 |
|--|--|--|---|---|---|---|--|---|--|--|--|---|---|---|--|-----------|--|---|---|
| | Db 6649 GACTGTTTGCAATCGCACACGTTTCTAAGGAGGTCATTCCATGCGCAAGATATCAGT 6708 QY 118 gggaatctgtatcaccattctccttagcctctccqtagtcctccaaggctgcaaggagtc 177 | 6709 GGGAATCIGCT | <pre>QY 178 cagtcactctctacatctcggggagaactcgctattaatataagagatgaaccccgttc 237 DD 6769 AACCCATCGGTCTCCAGCTACACAGTTGCTGTAAAGGTAAAAGATGATCCTGGCAC 6828</pre> | OY 238 tttagatccaagacaagtgcgacttctttcagaaatcagccttgtcaaacatatctatga 297 | | | Oy 418 tggogaccettaacagetgaagactttatagaatettggaaacaagtagetacteaaga 477 | Oy 478 agtctcaggaatctatgcttttgccttgaatccaattaaaaatgtacgaaagatccaaga 537 | aatgaatctacacttgttgt | OY 598 taccotggaatccccaacctcgcatttcttaaaacttttagctcttccagtcttttccc 657 Db 7156 CARTCTCCTCAACTCCAACTTCTAAAGCTGCTTACCCTCCCGTATTTATCC 7215 | Oy 658 egiteataaaleteaaagaaceetgeaateeaaatetetaaceaageggage 714 1 1 1 1 1 1 1 1 1 1 | Oy 715 tttctatcctaaaaatatcaaacaaaaacaatggataaaactctcaaaaaaccctcacta 774 Db 7276 TTTTTCTTAAAGAGAAAGACCAAGATGGTTAAAGCTAGAGAGAG | Qy 775 ctataatcaaagtcaggtggaaactaaaacgattacgattcacttcattcccgatgcaaa 834 | Oy 835 cacagcagcaaactatttaatcagggaaaactcaattggcaaggacctccttggggaga 894 Db 7396 AACIGCTTTATTCAACCAAGGAAGCTAGATTGGCAAGGTCTCCCTTGGGGACA 7455 | 895 7456 | 955 | 1015 | Y 1075 aggccgtgcaaaactgccgatcatctcctacctacaatattcatagctatcccgaaca 1134 | 1135 tcaaaaacaagagatggcacaacgccaagcttacgctaaaaaactcttaaagaagcttt |
| , | | _ | - 1 | <i>→</i> 1 | ~ 1 | → 11 | ٠ ـ ـ | 0 11 | 5 1 | 3 | J 1 | 0 1 | O D | Q P | S S | 9.y Db | δγ | QY Dp | δ |

0 bp DNA linear BCT 30-MAY-2000 39, section 43 of 94 of the complete tegaacatettaatettatettteeegtte 1254 en,C., Gill,S.R., Heidelberg,J.F., rson,J., Umayam,L.A., Utterback,T., ., Weidman,J., Khouri,H., Craven,B., .M., Nelson,M., DeBoy,R., Kolonay,J., Elsen,J. and Fraser,C.M. aagatcaccaaaaagctcggaattagtgtc 1554 Institute for Genomic Research, 9712 b. MD 20850, USA version replaced g1:7189472. CITTAGCIAAAICITIACIAGAAGAAGCICT 7746 ctccttatgcaatcaaccataaggacttcct 1494 atattattgagccgatctaccacgacgcatt 1614 no,C., Gill,S.R., Heidelberg,J.F., Son,J., Umayam,L.A., Utterback,T., Weidman,J., Khouri,H., Craven,B., M., Nelson,W., DeBoy,R., Kolonay,J., Eisen,J. and Fraser,C.M. ttgctcttctccaagcagacctatcttcagg 1374 tegeagactttgetgatectatggeatttet 1434 AACCITAIGCITTACAAGAICCICAATTIGA 8043 atctaggagtctcaccaacaggagttgtgga 1674 umydiaceae; Chlamydophila. tettttaateteg 1716 | |||| | |GTTTTACTCCG 8265 397-1406 (2000)

CDS

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FISFLGLGIQPPQASLGTLVKEGINAIDYYPWLFFFPSLIMIALSISFNLIGEGAKTL
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ATVAISGGKKIDFLMMRTTEILFSLPRIPIIILLLVIFHHGLLPLILAMTITGWIPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tanslation-"MFSTIKNRILFNLLSLMIVLTLFLVMKTIPGDPFNDEGCNVLS
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GLØSLFLSIGGGIALGTIAALKKKKQRRYILGASILQISIPAFIFATLLQYVFAVKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to SP:P24138 GB:X56347 PID:580897 GB:AL009126; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREKIFSTPKHTTTQDLLDAIPIFSLISTEMEPSEEYELQVASK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5946. .6800)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6831. .7775)
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/transl_table=11
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LVVLVWFFGDLLGISATTAALIGGELJITTNILDWOKDVIANTAMETFWFGALIMMA
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complement(2487. 2684)
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putative"
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                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="sodium:sulfate symporter family protein"
/dp_xrcein_id="AAF73687.1"
/db_xref="G1:8163459"
                                                                                         /note="synonym: Chlamydia pneumoniae AR39"
complement(197. .1609)
/organism="Chlamydophila pneumoniae AR39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
/protein_id="AAF28380.1"
/db_xref="GI:7189473"
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/product="hypothetical protein"
/protein_id="aAR38381.1"
/db_xref="GI:7189474"
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/protein_id="AAF38382.1"
/db_xref="G1:7189475"
                                                          'db_xref="taxon:115711"
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complement(1653. .2408)
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/gene="CP0562"
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/gene="CP0563"
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                                                                                                                                                                            complement(197. .1609)
/gene="CP0560"
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/transl_table=11
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/transl_table=11
                                                                                                                                                /gene="CP0560"
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PAT 06-FEB-2002
            12155 GCAGCCATTCTATTCAAACATAAGAAATTAGATTGGCAAGGACCTCCTTGGGGAGAACCT 12096
                                                                            12035 GCTTCGACTACATGGTTACTCTTTAATATACAAAAAAACCTTGGAACAATGCTAAATTA 11976
                                                                                                                                                                                                                                              11975 CGCAAGGCATTGAGCCTTGCAATAGACAAAGATATGTTAACCAAAGTGGTATACCAAGGT 11916
                                                                                                                                                                                                                                                                                                            11675 ACTATCCCTATAGTAGGCCAAGAGTTTTCACAATACAAAAAACTTCCTAGAGGGGAAC 11616
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                                                    899 attoctcaagaaaccctatccaatttacagtctaaggggcacttacactcttttgatgtc
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Chlamydophila pneumoniae
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Immunisation against Chlamydia pneumoniae
Patent: WO 0202606-A 128 10-JAN-2002;
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Sequence 128 from Patent W00202606,
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LSVFYGTLFMLSSLLSDLJQSIJDPQIRYAHGKEKKRK"
                                                                                                                                                                                                                                                                                  /LTGRS141.00="MXMHELKPTLKSLIPNLLFLLTLSSCSKQKQEPLGKHLVTAMS
HDLADIDPRNAYLSRDASLAKALYEGITRETDQGIALALARSYTLSKDHKVYFKLRP
SVWSOGPTGAYDEKSIKQLYFEBESPSIHTLLGVIKNSSAIHNAQKSLETLGIQAK
DDLTJVTTLEQPPFYFLTILARPVSVHHTLRESKKKGPPSFYISNOFPVIKHEH
ONYLLLEKNHHYYDHESVKLDFYTK II PDASTAFKLFREKSIDMIGSPWARPISNED
QKVLSQEKILTYSVSSTTLLIYNLQKPLIQNKALRKAIHALDKSSILRLVPSGQQEAV
TLVPPNLSQLNLQKBISTBERQTKARAYFQBAKETLSEKELABLSILKPIDSSNSSII
                                                                                                                                    clar to GB:M57689 SP:P24141 GB:X56347 PID:143603
identified by sequence similarity; putative"
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                                                                                                                                                                                                            /product="peptide ABC transporter, periplasmic peptide-binding protein" /protein_id="AAF38388.1"
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); Mismatches 682;
                                                                                                                                /note="similar to GB:M57689
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 409.8;
                                                              complement(8068. .9654)
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9
                                                                                                                                  Length 1584;
                                                                                                                              Score 409.4; DB 6; Length
Pred. No. 3.2e-89;
0; Mismatches 681; Indels
                                          /organism="Chlamydophila pneumoniae"
/db_xref="taxon:83558"
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S.p.A. (IT)
Location/Qualifiers
1. .1584
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                                                                                                                            Query Match 22.8%;
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BCT 26-MAY-2000
                   Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.

1 (bases 1 to 12173)
Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
cgtgcaaaaactgccgatcatctcctacctacaaatattcatagctatcccgaacatcaa 1138
                                                                               aaacaagagatggcacaacgccaagcttacgctaaaaaactctttaaagaagctttagaa 1198
                                                                                                                                                          1199 gaactccaaatcactgctaaagatctcgaacatcttaatcttatcttcccgtttcctcg 1258
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Read.T.D., Brunham.R., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Uttezback,T.,
Berry,K., Bass,S., Lihher,K., Weidman,J., Khouri,H., Craven,B.,
Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
Direct Stbmission
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                                                                                                 1024 GGGAAAAGACAAAAGAAATTCTTGAGGCTCAACAACTCTTTGAAGAGCTCTAGAC
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PIREEATLEFIEDAVYSHEPELPLSSQEEVRCHRPIILORGSKPAETPRFIAVGNSVV
ELVKVGMIGPMGRRGNVNPGQTLVRLWDELFALGRMGELVRLDGFCCKVLPATLGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MDSSCALKNLSSCEVSYRIPEVIATRKEVALVLIVLGTVLAAIG
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Vldhshiplatchryhilvhpgalavaamggihgfigrnapiitdsggegifslaygs
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DELLPPHTDPAYRQGSSQRTYAMBKRSLDYHLANGSYGSWYGVHGGTFPDGAKLGC
FVEDLPFOSAIGSSLGKNLRDIVGVVDYTANLSIERPRHLLGIGDLPSIMAYVGFG
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HLFKVHEDNAGIWASIHNMHYMQKIMSKIREKILNDQL"
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NTAGRLATURFFAFLAETTVKEVATCIRNNPGVDLTRLVFVLDFKGELQGFVTDRSLI
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LTGVALGILCGLVVCCMGCLGLGLFSTGGVQLGVTVSVGILGASLTATTLGVLSPFFF
AKIGVDPALASGPIVTALNDIMSMVIFLLITGTLNVLFFK"
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Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA On Jun 1, 2000 this sequence version replaced gi:7190506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:AL009126; identified by sequence
                                                                                                                                                                                                                                                                                             /note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                       /db_xref="taxon:83560"
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/db_xref="G1:8163227"
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/gene="TC0466"
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/codon_start=1
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/gene="TC0467"
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                                                                                                                                                                                                                                                                                                                                                                                               TSLTRIVCEYVGILLVICATICCRIAYLANGGLESER TLAITALSELVLIGGGIGVLCK
IARKIDVLYGEKIOPFAIRKWEOVILCEKRGGTIRPIQDPDMYMDYSLLDKOGGGIVLCK
VYTYPPAKARTAICRIACHLPTITTVYRVLYWAFRFLLIPFY VFOMIRGLYOEDLPF
EDQFFCSDIFFRENSERPVOAVKAPFYGVACYLASLYGLINPLSGRVIMASVERDWND
VIRSRGINGIFCEKNCLLEGGGTRSGLÖQHAWYLLGCFOPFRLFLLKDGEIVSGARPS
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FRPHLFSINQSQDLHIIYY"
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ASRAHLOIPRILAAVAODAEVSLEDVELISVANTPGLIGALSVGVNFAKGLASGLKK
TLIGVHVVAHLYAAVAODAEVSLEDVELISVANTPGLIGALSVGVNFAKGLASGLKK
GETPDKVARRELGEPPRGGGKLEELADGEDERAYPSRAKVSGNDFSFSGKTAVLYAL
KGNNSSAKAPFPEVSETOKRNIAASFOKAAPMIAGKLPDIVKAPSCESLIVGGGVAN
NRYFFRILNOTCSLPTYFPSSQLCSDNAAMIAGLGERIFCNQTYVSKEVIPCARYQNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALMSNODLITAHDEVERNADYLONRISITSFAFLPIDLSKDCGFFAKDNHTLVINLH
TPTPHFLKLLTLPVFTPVHPEHQIRNBAKALPISTGAFCLKEKKDRRUKLKIRNPYY
NKROYALOLEHIHVIPDOQTASALFKGGKLDWOGLPWGHSIPQEALATANKRRTPOSF
DISGTSWLTFNTSKVPFSPRKILOSALSLVLUKRALASAPFYKPARHLLPFHLBTYPEO
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LGITFPICGKEYALLQNDLTTNTFFWSINGWFADFSDPLAELSYFSSKGIKPYALQDP
LFDQLILSIETEKDPRKRISLSEASLYLEKONIIEPLYHDVFHYAANNKLSFVRLHP
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                                                                                                                                                                  /note="conserved hypothetical protein; identified by
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/protein_id="AAF73560.1"
/db_xref="GI:8163228"
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/db_xref="G1;7190511"
                                                           complement(4328. .5410)
/gene="TC0468"
                                                                                                             complement(4328. .5410)
                                                                                                                                                                                                     Glimmer2; putative"
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/transl_table=11
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6012. .7034
                                                                                                                                             /gene="TC0468"
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/gene="TC0471"
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/gene="TC0471"
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BEIJALINKRYGLDKPEFGYLIKLGLTLDFGESLIKTDRTVIGIITTALFSSAIL
GLESLCLALFGGITLGILAAFVRGGRTIFFSSIIGISVPAFVIGSFTATKY
LLPIRCWGDFSHLLLPSTALATFWRGGTTIFFSSIIGISVPAFVIGSFTOYIFNIKY
LLFIRCWGDFSHLLLASTALATAPMAFTTQLTYASVSASLKKDYVLLAYARGISPLKY
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9618. .10481.
                                                                                                                                                                                                                                          //orde="Similar to GB:M57689 SP:P24139 GB:X56347 PID:143606
PID:40007; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                    7;
                                                   /note="similar to SP:P24138 GB:X56347 PID:580897 GB:AL009126; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                              7009 GGGAATCTGCTTATCGCATTAGCAACAGCAATTACCGGCTGCTCCAAATCCTCCTC 7068
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                                                                                                      protein"
                                                                                                                                                                                                                                                                                       /product="peptide ABC transporter, permease protein"
                                                                                                                                                                                                                                                                                                                                                                                                            61 aaaattttcaaaaaaactctagtattcc---ggaaattcgtatatgcgcaagatatcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccgttctttagatccaagacaagtgcgacttctttcagaaatcagccttgtcaaacatat
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                                                                                                                                                                                                                                                                                                                           Length 12173;
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                                                                                                /product="peptide ABC transporter, |
/protein_id="AAF39320.1"
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                                                                                                                                                                                                                                                                                                                        Score 393.8; DB 1;
Pred. No. 1.7e-85;
0; Mismatches 702;
                                                                                                                                                                                                                                                                                                   /protein_id="AAF39321.1"
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8668. of 1
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/gene="TC0473"
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SGLVDMRYAKNS"
3668. .9612
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55.4%;
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7575 TCAGCAGACCGCTTCTGCTTCTAAACAAGAAATTGGATTGGCAAGGACTTCCTTG 7755 tatgaagcttagagaagccttagcatcagccttagataaggaagctcttgtctcaactat 1068 7876 TCCCAAGTIGCGACAAGCTITAAGCCITGTTCTAAATAAGGAAGCCTTAGCCTCCCAAC 7935 7987 AGAGCAACCTACTTACAAACAACAAGAAGCCGTCATTTTAGCCAAAACTCTGTTACAAGA 8046 agotttagaagaactccaaatcactgctaaagatctcgaacatcttaatcttatctttcc 1248 8166 tttagggttcgctatccctattgtcggaaaggaatttgctcttctccaagcagacctatc 1368 888 948 ttcagggaacttctctttagctacaggaggatggttcgcagactttgctgatcctatggc 1428 8227 CACCAACACTTTTTTATGTCCATAAACGGTTGGTTTGCAGACTTTTCCGATCCTTTAGC 8286 atttotaacgatotttgottatccatcaggagttoctcottatgcaatcaaccataagga 1488 1489 cttcctagaaattctacaaaaacatagaacaagagcaagatcaccaaaaacgctcggaatt 1548 8403 8287 CTTCTTGTCTGTTTTTTCTT---CTAAGGGAATCAAACCTTATGCCTTACAAGACCCTCT 8343 agigicgoaagcitcictitacciagagaccittcatattattgagccgatctaccacga 1608 8463 cgcatttcaatttgctatgaataaaaactttctaatctaggagtctcaccaacaggagt 1668 8464 retriticaciargececaariaaraaactitetitigitagatiacarecereageter 8523 tttccccgttcata---aatctcaaagaaccctgcaatccaaatctctacctatagcaag cggagetttetatectaaaaatateaaaacaacaatggataaaaeteteaaaaeeee 7576 AGGGGCTTTTTTTTTTTTAAAGAGAAAAAAGATCGCCGGTGGCTTAAATTAGAAAAAATCC tcactactataatcaaagtcaggtggaaactaaaacgattacgattcacttcattcccga 7636 CTATTATAACAAAGAGCAAGTIGCGATCCAGGAAATCCACATACATGTGATTCCTGA tgcaaacacagcagcaaaactatttaatcagggaaaactcaattggcaaggacctccttg gggagaacgcattcctcaagaaaccctatccaatttacagtctaaggggcacttacactc ttttgatgtcgcaggaacctcatggctcaccttcaatatcaatatccccctcaacaa tgttgttaccctggaatccccaacctcgcatttcttaaaacttttagctcttccagtctt 7936 CTT-----TGTTAAGCCCGCTAAACACCTACTTCCTACACACCTGCACACTTATCC 1129 cgaacatcaaaaacaagagatggcacaacgccaagcttacgctaaaaaactctttaaaga AGCGACATOTAGCGTCAACTCACAAATGGCCCCAAATGATGCGCGATCAATGGCGGAAGAAT tgtggacttccgttatgctaa 1689 1669 õ

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                                                                                                                                                                             Murdin,A.D., Oomen,R.P., Wang,J. and Dunn,P.
Chlamydia antigens and corresponding dna fragments and uses thereof
Patent: WO 0185972-A 5 15-NOV-2001;
Aventis Pasteur Limited (CA)
Location/Qualifiers
                                                                             PAT 30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                   /translation="muticlesscdetacalynedkqilaniiasqdihasyggvype
Lasrahlhippqvinkalqqaniljedmdilavtqtpglgigslsygyhpckgiaigak
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INEYFRSALQTACNLPVYFPPAKLCSDNAAMIAGLGGENFQKNSSIPEIRICARYQWE
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                                                                                                                                            Chlamydophila pneumoniae
Bacteria, Chlamydiales; Chlamydiaceae; Chlamydophila.
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100.0%; Pred. No. 1.4e-51;
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                                                                       Sequence 5 from Patent W00185972, AX300393
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||| || || || |||||| ||| 8524 TGTCGATATGCGGTATGCAAA 8544
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Matches 25
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                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                    REFERENCE
                                                                                                                                                                                 AUTHORS
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AX349505
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                                                                                                                                                                                                                                                                                                                                                                                  Length 1587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                      /organism="Chlamydophila pneumoniae"
/db_xref="taxon:83558"
                          l (sites)
Ratti,G. and Grandi,G.
Immunisation against Chlamydia pneumoniae
L Patent: WO 0202606-A 28 10-JAN-2002;
Chiron S.P.A. (IT)
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.1%; Score 181.4; DB 6; Best Local Similarity 49.3%; Pred. No. 1.1e-33; Matches 640; Conservative 0; Mismatches 626;
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| 2 CCTTCTTATCTATAACCTGCAAAAACCTCTAATACAAAATAAAGCCCTCAGGAAAGCCAT 941 | 0 agcatcagccttagataaggaagctcttgtctcaactatattcttaggccgtgcaaaac 1089 | 10 tgocgatcatctcctacctacaaatattcatagctatcccgaacatcaaaaacaagagat 1149 | ggcacaacgccaagcttacgctaaaaaactctttaaagaagctttagaagaactccaaat 120 | | | 0 tytoggaaaggaattigctcttctccaagcagacctatcttcagggaacttctttagc 1389 | tacaggagatgattcgcagactttgctgatcctatggcatttctaacgatctttgctta 1 | | | 6 | AX300389 1787 bp DNA linear PAT 30-NOV-2001 N Sequence 1 from Patent WO0185972. | | Chlamydophila | - | Murdin, A.D., Oomen, R.P., Wang, J. and Dunn, P. | Patent: WO 0185972-A 1 1 | 3 | or /db/ | 1011687 /note="unnamed protein product" | /codon_grart=1 /transl_table=11 /protein_id=CAD13017.1" | /db_xref="G1:17381781" // // // // // // // // // // // // // | HDLADLDPRNAYLSRDASLAKALYEGITERTDQGTALALAESYLSKDHKVYTFKLRP SVWSDGTPLTAYDFEKSIKQLYFEEFSPSIHTLIGVTKNSRAHMOKKIFTLRP | DDLTLVITLEQPFPYFLTLIARPVFSPVHHTLRESYKKGTPB5TYTSNGFPKKHEH QNYLILEKNPHYYDHESVKLDRVTLKIIPDASTATKLFKSKSIDWIGSPPRAPISNF | QKVLSQEKTLITSVSTTLLIYNLQKPLIQNKALRKATAHAIDRKSILRLYPSGQEAV TLVPPLNLQKETSTERGYTERGYTKAYPQEAKETLSEKELAELSILYPIDSSNSSII AOPTODOLY DONING THE TOWNSTONES | NELEARVERDU LIGIALI LÜÇİRLI HÜLLEKRRRÇĞDFFI ATGGWI AEYVSPVAFLSILGN PROLOGORUM PROLOGORUM KANDAYKENLEKRAĞMI I EBETPI I PLYHÇKYIYA HIPKI OMRUCCI I CHANDE KANDAYATA | 628 a |
| Db 882 | Qy 1030 Db 942 | Qy 1090 Db 997 | Qy 1150 Db 1056 | OY 1210 Db 1110 | Qy 1270 Db 1170 | Oy 1330 Db 1230 | Qy 1390 | | Db 1350 | T 389 | LOCUS DEFINITION ACCESSION | VERSION | SOURCE | REFERENCE | AUTHORS | JOURNAL | FEATURES Source | | SCDS | | | | | | | BASE COUNT ORIGIN |

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271 AAGCAGAGATGCTTCCCTAGCAAAAGCCCTCTATGAAGGACGACGACGACAAGAAACTGATC- 329
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                                                            202 agaactogctattaatataagagatgaaccccgttctttagatccaagacaagtgcgact 261
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                                                                                                                        262 tctttcagaaatcagccttgtcaaacatatctatgagggattagttcaagaaaataatct
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Pred. No. 1.1e-33;
                                0; Mismatches 626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, R., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Direct Submitssion
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
1210 cactgotaaagatotogaacatottaatottatotttocogtttootogtoagoaagtto 1269
                                          1210 TTCTGAAAAAAAACTCGCAGAACTCAGCATCCTCTATCCTATAGATTCCTCGAATTCCTC 1269
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                                                                                                                                    1270 CATCATAGCTCAAGAAATCCAAAGACAACTTAAAGATACCTTAGGATTGAAAATCAAAAT 1329
                                                                                                                                                                                    1330 tgtoggaaaggaatttgetetteceaageagaectatetteagggaaettetettage 1389
                                                                                                                                                                                                                                 1330 CCAAGGCATGGAGTACCACTGCTTTTAAAGAAACGTCGTCAAGGAGATTTCTTCATAGC 1389
                                                                                                                                                                                                                                                                                1390 tacaggaggatggttcgcagactttgctgatcctatggcatttctaacgatctttgctta 1449
                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 11402)
Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L., Utterback, T.,
Bowman, C., Bases, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,
McClarty, N., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GP:2444077; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE002313 11402 bp DNA linear BCT 26-NA
Chlamydia muridarum, section 44 of 85 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: Chlamydia trachomatis MoPn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia muridarum
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="phospholipase D family protein"
/protein_id="AAF39294.1"
                                                                                                                                                                                                                                                                                                                                                                             1450 tecateaggagtteeteettatgeaateaaceataagga 1488
                                                                                                                                                                                                                                                                                                                                                                                                                     1450 CĆCCAGAGACCTCAĆAATGGAGAAACAGTGATTACGA 1488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:83560"
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/transl_table=11
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/gene="TC0440"
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250. .1569
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AE002313.1 GI:7190484
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VERSION
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SOURCE
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JOURNAL
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RVRKPGAPRVHVKMCYIDNKILICGSANWSSACLTRNREDLFVIRGLTETQRQSLSEI
WQSVEEKTEPLTAQSLKRPREEEDDPGEGTSSGISSAGASAKKAKTQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLKYAIITRDFASFDRIMATVQCHRHPPGGIONENDLMLVLQNYIKQCIODNIIYTEV QONIRIAYVIYPSIKPLEARLELYDLFSRASQLFLSQCITLRFLNCFNKTGSSNLQQS QONIRIAYVIYPSIKPLEARLELYDLFSRASQLFLSQCITLRFUCHHYYENGFGCEA TQARSEBASSWLDEAASFPPNLEVGLOSAGABESCPEAAPTKLTSCYHAYENGFGCEA HAGEGTELYLLYDYDTOALDIOARTAHGFGETHYPYTHAIOEKNITLYMAPAINLYLGASLHQYSGLEKISKTMINNLDEHPFFALFRDHKLSVTLSSDNRQMGGTSVQNTMLLLSGFFSADEBDSHLTHVTSSPLTFKEIIQLNVEAIVSSPRDMCATSVQNTMILLSGFFSADEBDSHLTHVTSSPLTFKEIIQLNVEAIVSSFVDVDTKIMLLNSTHEYLSTYKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="GMP synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTPIVFYPSELFKGLADQDAFHTEIRNSHCDCVVVPPKDFFVIASSQHCFIAAIECPK
KKLFGLQFHPEVSDSQDIGDKILSNFVKHICQTSETWKIETIEKOLIOGIREKVGETE
RVLLGLSGGVDSSYLAVLLHNALGDRLSCVFVDTGLLRKNEVEEVKQQFSSLGIEILV
VDASEKFFHDLSGIEDPEQKRKYIGAAFIEVFDEASKNLDVQWLAQGTIYSDVIESAK
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PGLGVRVLGEVRREYVEIVKNADSIFIEELKKANLYHKVSOAFAVFLPCKSVANKGDC
RHYGYTIALRAVESTDFWIACWPSLSREFLNRCSSRIINEIPEVCRVYDISDKPPAT
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GVDAVKVGIGPGSICTTRIVSGVGLPQLTAIMDVAEALHDSSVRIIADGGMRYSGDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KALAAGAHCVMLGSMLAGTDEAPGETVQINEHSYKNYRGMGSLGAMKKGSAERYFOKN
NAKKFVPEGVPGLVPYKGSLHDVLYQILGGIRSGMGYLGAHNLEELRQNAVFSRITHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MREALTFDDVLLVPQYSEVLPQDACLTSSVSESLSLTIPILSAA
                                                                                                                                                                                                                                    /note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAF39295.1"
/db_xref="G1:7190486"
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                                                                                        complement(1661. .3049)
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/gene="TC0442"
                                                                                                                                                                complement(1661, .3049)
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/gene="TC0442"
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EITLEHPSSHFLETLTHPWFYPWARSKRSKELPIISMOPFIIRCYPDONEL
LLDKNWFYTBOKNYSLOAVRLOIVPDIHTAVOLFØKKYVDLVGLPWSSSFPLEEØKNL
SQDFLYDYPYLOKNYSTLOAVRLOIVPDIHTAVOLFØKKYVDLVGLPWSSSFPLEEØKNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MPKKKFLYILIPFLSLTFGLT/SCHQKEENLRNILKVAICHDPMS
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GSABYTRUSINDVNLHANTOSIOLOGALNEBATORSYLVYTIIIDSLESGOOTI
DILKALGSKLRVRVGTGDRIHCKACILLDALNEBATORSVLYTIIIDSLESGOOTI
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                                                                                                                                                                                           /note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="peptide ABC transporter, periplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="phospholipase D family protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide-binding protein"
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/gene="TC0445"
                                                                                  complement(6896. .7135)
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7407 IGTIGCIATITGCCACGAICCAATGICITIAGAICCICGCCAAGITITITIGAITAAAGA 7466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8001 TITAGAIGCIGIACGCITACAAATAGIICCCGATATICATACAGCGGIGCAATIGITICA 8060
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                                                                                                                                                                                                                                                                                                                                                    271 aatcagccttgtcaaacatatctatgagggattagttcaagaaaataatctttcaggaaa 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatagageetgetettgeagaagactactetetteeteggaeggaeteaettatacttt 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    taaactgaaatcagctttttggagtaatggcgaccccttaacagctgaagactttataga 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 atcttggaaacaagtagctactcaagaagtctcaggaatctatgcttttgccttgaatcc 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caccttcaatatcaataaattcccctcaacaatatgaagcttagagaagccttagcatc 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agcettagataaggaagetettgteteaaetatattettaggeegtgeaaaaetgeega 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    571 ototoctaatgaatotacacttgttgttaccctggaatccccaacctcgcatttcttaaa 630
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                                                                                                                                                                al Similarity 711; Conserv
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Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                          331
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/gene="trpA"
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Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W., Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.

Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
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Stephens.R.S., Kalman,S., Lammel,C.J., Fan,J., Marathe,R.,
Aravind,L., Mitchell,W.P., Olinger,L., Tatusov,R.L., Zhao,Q.,
Koonin,E.W. and Davis,R.W.
Direct Submission
Submitted (20-MAY-1998) Program in Infectious Diseases, University
of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
Location/Qualifiers
1156 acgccaagcttacgctaaaaaactctttaaagaagctttagaagaactccaaatcactgc 1215
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Genome sequence of an obligate intracellular pathogen of humans:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis section 18 of 87 of the complete genome.
AE001291.1 GI:3328573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8703 TCGACTTTTGGTTGAGGATTCAACAGATTTACAAATTCTAGCAGAACAACTATTGGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 10827)
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Science 282 (5389), 754-759 (1998)
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AUTHORS
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gene

CDS

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FSKREKFRYLTQAKPSLLTKKIQLTKTPFDETIETAFSHIREGLYLSESEQRDHDKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4256 ATTGCGATCTGTCATGATCCAATGTCTTTAGATCCGCGTCAGGTTTTTTTAAGCAAAGAT 4315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4430 TITCTAAAAAATACATICTGGAGCAACGGAGATGTTGTAACAGCATATGATTTTGAAGAG 4489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4490 ictatiaaacaaartatrocaagaaartgaraaccerrograaceercrecarra 4549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 attaatataagagatgaaccccgttctttagatccaagacaagtgcgacttcttcagaa 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4550 ATTARARATICICAIGCIGITITAACAGGAGCICICCCIGITGAAGAITIAGGIGITAGA 4609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4610 GCTITGAATGCGAAAACTCTAGAAATTGTTTTAGAAAACCCGTTTCCTTATTTTCTAGAG 4669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 atcagccttgtcaaacatatctatgagggattagttcaagaaaataatcttcaggaaat 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaactgaaatcagctttttggagtaatggcgacccttaacagctgaagactttatagaa 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4730 AAGCGTAACAAACGCGTTTTCCCGATAATTTCTAATGGTCCTTTTGCGATTCAATGTTAT 4789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4790 GAGCCCCAAAGATATTTACTAATCAACAAAACCCTCTGTATCATGCCAAGGACGATGTT 4849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 attaaaaatgtacgaaagatccaagagggacacctctccatagaccattttggagtgcac 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 totoctaatgaatctacacttgttgttaccctggaatccccaacctcgcatttcttaaaa 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---accetgcaatccaaatctctacctatagcaagcggagctttctatcctaaaaatatc 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adacaaaaacaatggataaaactctcaaaaaaccctcactactataatcaaagtcaggtg 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      794 gaaactaaaacgattacgattcacttcattcccgatgcaaacacagcagcaaactattt 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcttggaaacaagtagctactcaagaagtctcaggaatctatgcttttgccttgaatcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 10827;
                                                                                                                                                                                                                                                                                                                                                                                                                                 6.5%; Score 117.6; DB 1; -
... Pred. No. 3.3e-18;
...hres 754; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632 cttttagctcttccagtcttttccccgttcataaatctcaaaga-
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                                                                                                                                                                                                                                                                                                                                                                                                                   LDPRQVFLSKDVSIVKALYEGIVREKEAAFQLALAERYHOSDDGCVYTFFLKNTFWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIVLENPEPPYELEILAHPYFYPVHTSIREYYKDKRNKRUPFIISNGPFAIOCYEPORY
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AAILLSQLFLTNYEGVCLTVAPVFSLAFFYDBIRAWNYISONYSNRKOLAITAFYGS EYYKESLEWEERSVLPFSQACKOAFAGLSFPLNLIFACIFS FFYVOLNANLSIPDTCR FFVNSACWFILVLSIFSFRAESLRHLRWLSLLFAAGIILSPVIFHLPLEASTLLSIIVS

854 aatoagggaaaactcaattggcaaggacctccttggggagaacgcattcctcaagaaacc 913

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source
                                      TITLE
JOURNAL
                     AUTHORS
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                               4970 CARAGAAATCTCC---CTAGAGAAAATTATTTGATTATCCTGTATTGAGTTGCTCTGTT 5026
                                                                   ctcacettcaatatcaataaattcccctcaacaatatgaagettagagaagccttagca 1033
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914 ctatecaatttaeagtetaaggggeaettaeaetettttgatgtegeaggaaeeteatgg 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 9364)
Gominet,M., Slamti,L., Gilois,N., Rose,M. and Lereclus,D.
Oligopeptide permease is required for expression of the Bacillus
thuringiensis ploR regulon and for virulence
Mol. Microbiol. 40 (4), 963-975 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1454 tcaggagttcctccttatgcaatcaaccataaggacttcctagaaattctacaaaacata 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5551
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Bacillus thuringiensis
Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus/Staphylococcus group.
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                                                                                                                                       tcagcettagataaggaagetettgteteaactatattettaggeegtgeaaaaaetgee
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ALISBFVDKFRQSSEFHTRKEAGVAXLRFNQSNQYLSNKNLRKAISMSFDRDNIAKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNNGAIGAYGFYGKDFAEGPNKKDFRAENGKLYETNPKEAKKLWETAKKELGTDKIEL
BFLNFDNEDAKKYGEFLKGEMEKNLPGISIKIKQQPPAGKNKLEDSQQYDIAFGIWGP
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EDAVITPIFQKGSAYIYKDAVKDIIPINYGGRLTYKWASVEQK"
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OAILIGFFIGLILGIVALRINTWVDYGATISVLGMSVPSFVFAALLOYFVGKLGL
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VKHALRNALIPVYTILGPMVAALITGTLVTESDIYAVPGLGEQFVKSITVNDYTVIMGT
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Gominet,M., Gilois,N., Rose,M. and Lereclus,D.
Direct Submission
Submitted (13-SEP-2000) Biotechnologies, Institut Pasteur, 25
du Docteur Roux, Paris 75015, France
                                                                                                                                                                                                                                        'gene="oligopeptide permease operon"
                                                                                                                                                         /organism="Bacillus thuringiensis"
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1567 c 1818 g 2714 t
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PDLLKPPKGDAFAPRNPQALKIDFEMDPPLFKVSDTHYAATWLHEQAPEVKPPAVVE
KRILQMKAGEQHD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 ttttaaact---gaaatcagctttttggagtaatggcgacccttaacagctgaagactt 444
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Pred. No. 6.1e-09;
0; Mismatches 389; Indels 9
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6112. .7047
                                                                                                                                                                                                                                                                                                                                                              4.48;
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Matches 352; Conservative
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2009 IGATIGGAAACATGAGCAAAGCTICCAGTITAAGAAGCAACCCAICATATIGGGAAAAAAA 2068

742 acaatggataaaactctcaaaaaaccctcactactataatcaaagtcaggtggaaactaa 801

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2186 GITTAGACAAAGCTCAGAATTCCACACAAGAAAGAAGCAGGGGTTGCTTACCTAAGAIT

Search completed: July 26, 2002, 04:36:20 Job time: 5828 sec

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  RESULT
                                                                                                                                                           July 26, 2002, 03:00:52; Search time 299.98 Seconds (without alignments) 10296.450 Million cell updates/sec
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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/*tag= a
/product= "ATP-binding cassette protein"
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2020
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WPI; 2001-648549/74. P-PSDB; AAE12212.

for DNA molecule 1 1s in mammals, יייי טוגמוויטלביי טוגמוויטלביים אוף-Dinding cassette and corresponding DN preventing, diagnosing and treating Chlamydia infections particular humans

Claim 2; Fig 1; 88pp; English.

The present invention relates to novel Chlamydia pneumoniae ATP-binding cassette protein and its corresponding gene. Sequences of the invention are useful for detecting chlamydia infection by assaying a body fluid of a mammal with the components. They are also used as vaccines. Ampliating of a mammal with the components. They are also used as vaccines. Ampliating cassette antibodies and vaccines of the invention are useful for preventing or treating Chlamydia Infection eq. infection caused by c. trachomatis, c. psittaci, c. pneumoniae or c. pecorum in mammals, as humans. The nucleic acid molecules are useful for producing as poxyluses, which are further useful for preventing and/or treating as poxyluses, which are further useful for preventing and/or treating strains that can over-express the nucleic acid molecules or express it in a non-toxic, mutated form. The present sequence is a gene encoding chlamydia pneumoniae ATP-binding cassette.

Sequence 1799 BP; 560 A; 439 C; 294 G; 506 T; 0 other;

ö 180 180 300 360 360 420 420 480 540 Gaps 009 900 octggaatccccaacctcgcattcttaaaacttttagctcttccagtcttttccccgt 660 9 9 1 acttccccctgctaaactatgctcagataatgctgctatgattgcaggtctagggggag 121 aatotgtatcaccattctccttagcctctccgtagtcctccaaggctgcaaggagtccag 121 aatctgtatcaccattctccttagcctctccgtagtcctccaaggctgcaaggagtccag tcactcctctacatctcggggagactcgctattaatataagagatgaaccccgttctt attagttcaagaaaataatctttcaggaaatatagagcctgctcttgcagaagactactc tctttcctcggacggactcacttatacttttaaactgaaatcagctttttggagtaatgg agatecaagacaagtgegaettettteagaaateageettgteaaacatatetatgaggg ctcaggaatctatgcttttgccttgaatccaattaaaaatgtacgaaagatccaagaggg acacetetecatagaceattttggagtgeactetectaatgaatetacaettgttgttae ctcaggaatctatgcttttgccttgaatccaattaaaaatgtacgaaagatccaagaggg cgacccettaacagetgaagaetttatagaatettggaaacaagtagetaeteaagaagt DB 22; Length 1799; .; Indels ; 0 s; Score 1799; I s; Pred. No. 0; 0; Mismatches 100.0%; 100.0%; Matches 1799; Conservative Match Local Similarity 181 181 241 301 301 361 361 421 421 481 541 541 481 £09 Query 1 Best L ò g Q q ò qq qq 8 δ δ δŽ à a à 8 δ ò g δŽ 2 ò

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                                                                                                                                                                                                                                                               Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
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                                                                                                                                                                                                                              Nucleotide sequence of the complete genome of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 1230025;
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                                                                                                                                                                                                                                                                                     sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss.
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: Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae
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                                                                                                                          AAX91990 standard; DNA; 1230025
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99.98;
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                      attagttcaagaaaataatctttcaggaaatatagagcctgctcttgcagaagactactc
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    tatocotattgtoggaaaggaatttgotottotooaagoagacotatottoaggaaott 1380
                                                                               ctttgcttatccatcaggagttcctccttatgcaatcaaccataaggacttcctagaaat 1500
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                     tatccctattgtcggaaaggaatttgctcttctccaagcagacctatcttcagggaactt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Open reading frames (ORFs) of the genome encode
                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome sequence of Chlamydia trachomatis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 373-656; 1755pp; English
                                                                                                                                                                                                                                                                                                                                    AA201425/c
ID AA201425 standard; DNA; 1038602
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97ER-0015041.
97FR-0016034.
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17-DEC-1997;
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polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines against chlamyda trachomatis. Antisense and ribosyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252080 GGGAATCTGCTTGCTCCTAGCATTAGCAACTTCTGGATGTTCAAAATCCTCTCTAACGC 252021
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                                                                                                                                                                                                                                                                                      conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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Pred. No. 2.4e-115;
0; Mismatches 696; Indels 50; Ga
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Matches 976; Conservative
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251393 AACTGCTTCTGCTTTATTCAACGAAAGCTAGATTGGCAAGGTCTCCCTTGGGAAA 251334
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Cacagcagaaactatttaatcagggaaaactcaattggcaaggacctccttggggaga
                                                                         acgcattcctcaagaaaccctatccaatttacagtctaaggggcacttacactctttga
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                                                                                                                                          ATP binding cassette; secretary locus open reading frame; endopeptidase;
                                                                                                                        Chlamydophila pneumoniae gene encoding an endopeptidase.
                                                                    AAS18752 standard; DNA; 1235
                                                                                                          (first entry)
                                                                                                         26-MAR-2002
                                                                                       AAS18752
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                                                          AAS18752
ID AAS1
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AC AAS1
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KW ATP
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The present invention relates to the isolation of Chlamydophila pneumoniae strain CML029 genes and their encoded proteins. The genes of the invention encode an APP binding cassette gene, a secretary locus open reading frame (ORF), an endopeptidase, a protease, a protease, a reprofesse, clp protease submit, a ransqlyoclase/transpeptidase, a CLP protease submit, a genes of the invention can be used in a vector as a vaccine for the prevention and treatment of Chlamydia infections. Also described are B- and T-cell epitopes from the proteins of the invention which can be used as Chlamydia antigens. AASI8750-AASI8759 represent the C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secretary locus ORF; protease; metalloprotease; CLP protease ATPase;
CLP protease subunit; transglycolase/transpeptidase; CLPc protease;
thioredoxin; Chlamydia infection; antibacterial; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine useful for immunising mammals against chlamydia infections, comprises vectors having sequences of ATP binding cassette gene, secretary locus open reading frame gene of chlamydia
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100.0%; Pred. No. 1.1e-61;
ive 0; Mismatches 0;
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                                                      Chlamydophila pneumoniae CWL029
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                                                                                                                                                                  2000US-202672P.
2000US-207852P.
2000US-211796P.
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2000US-211798P.
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2000US-235361P.
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2000US-212044P.
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Best Local Similarity
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                                                                                 WO200185972-A2.
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16-JUN-2000;
16-JUN-2000;
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26-SEP-2000;
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The present invention relates to the isolation of Chlamydophila pneumoniae strain CWL029 genes and their encoded proteins. The genes of the invention encode am ATP binding cassette gene, a secretary locus open reading frame (ORF), an endopeptidase, a protease, an endopeptidase, a repression it, a metalloprotease, CLP protease ATPRASE, a CLP protease subunit, a perangproclase, transpeptidase, a CLP protesse, or thioredoxin. The genes of the invention can be used in a vector as a vaccine for the prevention and treatment of Chlamydia infections. Also described are B- and T-cell epitopes from the proteins of the invention which can be used as Chlamydia antigens. AAS18750-AAS18759 represent the C. pneumoniae
                                                                                                                                                                                                                                                                                                                         endopeptidase;
                                                                                                                                                                                                                                                                                                                                         Secretary locus ORF; protease; metalloprotease; CLP protease AlPase; CLP protease subunit; transglycolase/transpeptidase; CLPc protease; thioredoxin; Chlamydia infection; antibacterial; ds.
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                                                                                                                                                                                                                                              Chlamydophila pneumoniae gene encoding an ATP-binding cassette.
                                                                                                                                                                                                                                                                                                            binding cassette; secretary locus open reading frame;
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16-JUN-2000; 2000US-211798P.
16-JUN-2000; 2000US-21180IP.
16-JUN-2000; 2000US-212044P.
26-SEP-2000; 2000US-23535P.
26-SEP-2000; 2000US-23536IP.
                                                          AAS18750 standard; DNA; 1787
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BP. DNA; 1536 AAX61764 standard; AAX61764 AAX61764

(first entry)

19-JUL-1999

Antigenic protein; vaccine; Lyme disease; infection; detection; ss. burgdorferi antigenic protein coding sequence, t606.nt. 97US-0057483. 97US-0050359. 97US-0053344. 97US-0053377. 98WO-US12718. Borrelia burgdorferi. WO9859071-A1 18-JUN-1998; 22-JUL-1997; 22-JUL-1997; 03-SEP-1997; 30-DEC-1998 20-JUN-1997

Hanson MS, GENOME SCI INC Erwin AL, MEDIMMUNE (HUMA-) HUMAN Choi GH, (MEDI-)

New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease Lathigra R; WPI; 1999-189980/16. P-PSDB; AAY20067

Claim 1; Page 182-183; 275pp; English.

This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for the Borrelia genus. The products can also be used for the Borrelia genus.

Sequence 1536 BP; 631 A; 246 C; 256 G; 403 T; 0 other;

6 290 atctatgagggattagttcaagaaaataatctttcaggaaatatagagcctgctcttgca 349 350 gaagactactctttcctcggacggactcacttatacttttaaactgaaatcagctt- 408 54; Length 1536; Indels Score 74.6; DB 20; Pred. No. 1.1e-10; 0; Mismatches 639; 4.18; Conservative Similarity 602; Query Match Local Best Loca Matches á g ò g

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              This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 aaagggtgggatatttcttctgatggaacagtttacacatttaacctaagagaaaaatc 291
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Query Match Best Local Similarity

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gatcaccaaaaacgctcggaattagtgtcgcaagc 1560
                                1402 gatccaataaaaagacaagacattttaagacaagc 1436
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Enterococcus faecalis EF027 gene fragment. AAX20051 standard; DNA; 1028 BP (first entry) 20-APR-1999 AAX20051; AAX20051 ID AAX2

Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic; ss.

Enterococcus faecalis,

WO9850554-A2

12-NOV-1998

98WO-US08959. 04-MAY-1998; 14-NOV-1997;

97US-0066009. 97us-0046655. 06-MAY-1997; 16-MAY-1997;

(HUMA-) HUMAN GENOME SCI INC.

Kunsch CA; Hromockyj A, Choi GH, Bailey C,

WPI; 1999-070095/06.

P-PSDB; AAY00061

New isolated Enterococcus faecalis polynucleotides - used to develop lucts for the detection of Enterococcus and for use in vaccines prevention or attenuation of Enterococcus infection products

Claim 1; Page 107-108; 301pp; English.

The present sequence encodes an antigenic polypeptide fragment isolated from Enterooccus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nuclectide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein activity

Sequence 1028 BP; 350 A; 174 C; 234 G; 269 T; 1 other;

ö 431 acagctgaagactttatagaatcttggaaacaagtagctactcaagaagtcccaggaatc 490 371 gacggactcacttatacttttaaactgaaatcagctttttggagtaatggcgaccctta 430 317 agcagtaatcaaatggatatttttaaaaatgggcgtgcggtgcgggaaggacaagccacg 376 Gaps 257 aaagcaggggattttgtagttgcgtttagaaacgtggtcgatccagcatacggttcaagt 491 tatgettttgeettgaatecaattaaaaatgtaegaaagatecaagagggaeaeetetee 0; Length 1028; Indels DB 20; 0; Mismatches 147; Score 63.8; DB 28 3.5%; 152; Conservative Local Similarity Query Match Matches qq ŏ δλ qq δy Q

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377 atggaagaatttggtgtcaaagcaatcgatgaccagacactagaactaacattggaaaat 436
 atagaccattttggagtgcactctcctaatgaatctacacttgttgttgttaccctggaatcc 610
                                                   New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                     ccaacctcgcatttcttaaaacttttagctcttccagtcttttccccgttcataaatc
                                                                                                                                                                                    Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                  Enterococcus faecalis genome contig SEQ ID NO:380.
                                                                                                                                                                                                                                                                                                                                                       CA;
                                                                                                        AAX13317 standard; DNA; 1121 BP.
                                                                                                                                                                                                                                                                                                                                                       Kunsch
                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                             97us-0066009
                                                                                                                                               (first entry)
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                                                                                                                                                                                                                 Enterococcus faecalis.
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16-MAY-1997;
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                                                                                                                            AAX13317;
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551
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                                                                                                AAX13317
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Entercococus faecalis genome. AAXI2938 to AAXI3919 represent these nucleotide sequences which are Primary nucleotide sequence. The conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting of the conting conti

Claim 1; Page 1556; 2084pp; English.

Sequence 1121 BP; 375 A; 186 C; 263 G; 296 T; 1 other;

0; Length 1121; Indels 20; Score 63.8; DB 20, Pred. No. 1.1e-07; 0; Mismatches 147, 3.5%; 50.8%; Conservative Similarity Best Local Sim: Matches 152; Query Match

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371 gacggactcacttatacttttaaactgaaatcagctttttggagtaatggcgaccctta 430 281 gacgggttagtctatacattcaagttacgagaagcaaaatggacaaacgggggtccagtt 340 δλ Dp

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AAA51864;
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ID AAA5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a gene isolated from Enterococcus faccalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faccalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be sequences can be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
431 acagetgaagaetttatagaatettggaaacaagtagetaetcaagaagteteaggaate 490
               atagaccattttggagtgcactctcctaatgaatctacacttgttgttaccctggaatcc 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
                                                                                                                                                         ccaacctcgcatttcttaaaaacttttagctcttccagtctttttccccgttcataaatc 669
                                                                                                                                                                        New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
                                                                                                                              461 atggaagaatttggtgtcaaagcaatcgatgaccagacactagaactaacattggaaaat
                                                     tatgettttgeettgaateeaattaaaaatgtaegaaagateeaagagggaeacetetee
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                                                                                                                                                                                                                                                                                                                                                                         detection; attenuation; antigenic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bailey C, Choi GH, Hromockyj A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 107; 301pp; English
                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis gene EF027.
                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                     AAX20050 standard; DNA; 1122
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97US-0046655.
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16-MAY-1997;
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3.5%; Score 63.8; DB 20; Length 1122; llarity 50.8%; Pred. No. 1.1e-07; Conservative 0; Mismatches 147; Indels 0;

Query Match Best Lócal Similarity Matches 152; Conserv

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/product='ligand-binding_protein
/transl_except= (pos:2106..2107,aa:Phe)
/note= "this codon contains an apparent 1 base deletion
which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                       Opp operon; SpoOK; oligopeptide permease; sporulation; ABC transporter; ATP-binding cassette transporter; mutation; protein production; oppA; oppB; oppE; oppE; ds.
             550
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                                              acagetgaagaetttatagaaatettggaaacaagtagetaeteaagaagteteaggaate 490
                                                                                                                  400 agcagtaatcaaatggatatttttaaaaatgggcgtgcggtgcgggaaggacaagccacg 459
gacggactcacttatacttttaaactgaaatcagctttttggagtaatggcgaccctta 430
                                                                                                                                                                 460 atggaagaatttggtgtcaaagcaatcgatgaccagacactagaactaacattggaaaat 519
                                                                                                                                                                                      611 ccaacctcgcatttcttaaaacttttagctcttccagtcttttccccgttcataaatc 669
                                                                                                                                                                                                       491 tatgottttgoottgaatocaattaaaaatgtacgaaagatocaagagggacacototoo
                                                                                                                                        551 atagaccattttggagtgcactctcctaatgaatctacacttgttgttaccctggaatcc
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                                                                                                                                                                                                                                                                        AAA51864 standard; DNA; 6300 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENENCOR INT INC. (DIAZ/) DIAZ-TORRES M.
                                                                                                                                                                                                                                                                                                                                               B. subtilis opp operon.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
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(FERR/) FERRARI E.
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ŭ Ferrari Diaz-Torres M,

2000-452412/39

P-PSDB; AAY97040, AAY97041, AAY97042, AAY97043, AAY97044

Production of proteins, such as hormones, enzymes, growth factors or cytokines, in gram-positive microorganisms containing a mutation in at least one of the genes of the opp operon gene cluster

Disclosure; Fig 1A-M; 32pp; English.

The opp operon of Bacillus (also known as spook operon) encodes an oligopeptide permease that is required for the initiation of sporulation and the development of genetic competence. The opp operon is a member of the family of ATP-binding cassette (ABC) transporters involved in the import or export of oligopeptides from 3-5 amino acids. Bacillus strains containing a mutation in the opp operon produce more recombinant protein than the wild-type strain. Therefore, gram-positive microorganims, especially Bacillus strains, containing a mutation in at least one of the genes of the opp operon can be used for heterologous protein production, especially hormones, enzymes (preferably proteases such as subtilisin), growth factors or cytokines.

Sequence 6300 BP; 1919 A; 1222 C; 1462 G; 1697 T; 0 other;

5 1044 tatatgccgatcaataagaaaattgcagagaaaaataaaaatggaatacaaatgccgga 1103 tgggccggtatgccgctcggacagc -- ttccgacagaatccctgccgaccctgaaaaa 1340 actetegaaaaaaatgaeeagtattgggataaagaeaaagteaaactgaagaaaategat 1223 atccaagagggacacctctccatagaccattttggagtgcactctcctaatgaatctaca 589 cttgttgttaccctggaatccccaacctcgcatttcttaaaacttttagctcttccagtc 649 aaggggcacttacactcttttgatgtcgcaggaacctcatggctcaccttcaatatcaat 991 Gaps 410 tggagtaatggcgaccccttaacagctgaagactttatagaatcttggaaacaagtagct 804 tggtctaatggagaccctgtaactgcacaagattttgaatatgcttggaaatgggcgctt gaccctaataatgaatcacaatacgcttaccagctctactacataaaaggtgctgaagcg gatgattatgtatcaaacgggccgttcaaaatgacggcatggaaacacagcggctctatt 470 actcaagaagtctcaggaatctatgcttttgccttgaatccaattaaaaatgtacgaaag 1224 atggttatgatcaacaataacaatacggaactaaaaaaattccaagctggcgaacttgat gcgaataccggaaaaggcagcctagacgatgtggcagtaaaagctgtgaatgacaaaacg aaactctcaaaaaaccctcactactataatcaaagtcaggtggaaactaaaacgattacg attoacttcattcccgatgcaaacacagcagcaaaactatttaatcagggaaaactcaat tggcaaggacctccttggggagaacgcattcctcaagaaaccctatccaatttacagtct ---atctcaaagaaccctgcaatccaaat-----27; Length 6300; Indels Score 63.6; DB 21; Pred. No. 2.8e-07; 0; Mismatches 724; 3.5%; Similarity 43.4%; ttttccccgttcataa----575; Conservative Query Match Local Matches 1104 1164 1284 864 924 984 650 590 752 812 872 932 à q δò a à g ŏ QQ ã Q δŽ q g οž ŏ g ò QD δy

98WO-US08959

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1341 gacggttctttacatgttgagccgattgcaggagtgtattggtacaaattcaacactgaa

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1401 gctaagccattagacaacgtcaatatccgtaaagctttaacatattcgcttgaccgtcag 1460 getettgteteaactatattettaggeegtgeaaaaactgeegateateteetaeetae 1111 1461 tegattgttaaaaaegttaegcaaggagageaateeeggeaatggetgeagtgeegeet 1520 gcaaaagaataccttgaaaaaggcctaaaagaaatgggcttaagcaaggcatctgatttg 1640 1701 caagaaatgiggaagaaaaatttaggcgtigatgtigagcttgatactcagagiggaat 1760 1521 acaatgaagggatttgaggataacaaagaaggatacttcaaagacaatgatgtcaaaaca 1580 catcttaatcttatctttcccgtttcctcgtcagcaagttctttactagtccaacttata 1288 cttctccaagcagacctatcttcagggaacttctctttagctacaggaggatggttcgca 1408 1761 gictatatigataagciccacagccaagatiatcaaatcggccgiaigggciggcicggc 1820 gactttgctgatcctatggcatttctaacgatctttgcttatccatcaggagttcctcct 1468 gacticaaigatectateaacticetigaatigticegegacaaaaaeggaggaaataae 1880 tatgcaatc---aaccataaggacttcctagaaattctacaaaaacatagaacaagagcaa 1525 gatcaccaaaaacgeteggaattagtgtegcaagettetettttaeetagagaeettteat 1585 2001 ccggttgccccaatctatttctatactgatacttgggtacaggatgaaaacctaaaaggt 2060 ctaggagteteaceaacaggagttgtggacttecgttatgetaaggaaaattageacete 1705 2061 gitaicaigccaggiaciggigaggittaiticagaaacgcaiattitaaaiaaggciac 2120 Enterococcus faecalis; infection; vaccine; immune response; diagnosis; aatattcatagctatcccgaacatcaaaaacaagagatggcacaacgccaagctta---c gctaaaaaactctttaaagaagctttagaagaactccaaatcactgctaaagatctcgaa cgagaacagtggaaaggaaagtttagggttcgctatccctattgtcggaaaggaatttgct ccaaaaatcaaattgtcttacaacactgatgacgcacacgcgaaaatcgctcaagcagta attattgagccgatctaccacgacgcatttcaatttgctatgaataaaaactttctaat 1941 gataaaaacaaaacgtgcagagctgctgaaaaaagcagaaggtattttcattgatgaaatg Enterococcus faecalis EF017 gene fragment. detection; attenuation; antiqenic; ss. AAX20031 standard; DNA; 1564 BP (first entry) Enterococcus faecalis, 1706 ttttaa 1711 2121 gtctga 2126 04-MAY-1998; W09850554-A2 20-APR-1999 12-NOV-1998 AAX20031; 1052 1581 1229 1349 1821 1881 1646 RESULT 12 1112 1169 1641 1289 1409 1526 1469 1586 AAX20031 a Qγ g QΥ qq QΫ 22 g qq g δŽ 2 Q δ Q ΩŸ Q QΣ g 셤 δŏ d δŏ g ŏ

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gcagctttgaaaattcgtgaaattcctggaacgtattatatccaattaaatacgcaaaaa 841
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                                                                                                                                                                                                                                                                                             The present sequence encodes an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic accids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 aaagatgcaaaatggagtaacggcgagccaatcacagcaaatgattttgaatactcttgg 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 aatgaatctacacttgttgttaccctggaatccccaacctcgcatttcttaaaactttta 637
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                                                                                                                                                                                      New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
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Pred. No. 2.8e-07;
0; Mismatches 399; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1564 BP; 555 A; 257 C; 341 G; 411 T; 0 other;
                                                                                                     Kunsch CA;
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                                                                                                   Hromockyj A,
                                                                                                                                                                                                                                                             301pp; English.
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97US-0066009.
97US-0044031.
                                                                  (HUMA-) HUMAN GENOME SCI INC
                               97US-0046655.
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                                                                                                 Choi GH,
                                                                                                                                  WPI; 1999-070095/06.
                                                                                                                                                                                                                                                            Claim 1; Page 96;
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                                 16-MAY-1997;
                                                                                                   Bailey C,
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Best Local Si
Matches 325;
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                                                                                                                  Entercoccous facealis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. facealis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Entercoccus genus in a namimal. They can also be used for detecting Entercoccus antibodies in a sample. The nucleotide sequences can be used for detecting Entercoccus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
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                                                                                                                                                   398 aaatcagctttttggagtaatggcgaccocttaacagctgaagactttatagaatcttgg 457
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                                                         842 gatottttggcaaataagaatgcacgtcgagcaatagcattatcattgaattctgagcgt
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Pred. No. 2.9e-07;
0; Mismatches 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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97US-0046655.
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al Similarity 44.7%;
325; Conservative (
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                                                                                                                                                                                                                              1115 attcata 1121
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995 ttccccctcaacaatatgaagcttagagaagccttagcatcagccttagataaggaagct 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                        ctagataaggtggatgtccaagtagttaaagaagtcaatactgggaaaaatcttttcgaa 795
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                               aaacaagtagctactcaagaagtctcaggaatctatgcttttgccttgaatccaattaaa
                                                            aagogcacagtggacccaaaaaaagcttccccgcaagcgtattactttgaagggttaaaa
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                                                                                           aatgtacgaaagatccaagagggacacctctccatagaccattttggagtgcactctcct
                                                                                                                                                        aatgaatctacacttgttgttaccctggaatccccaacctcgcatttcttaaaaactttta
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AXI2938 to AXX1319 represent these nucleotide sequences which are primary nucleotide sequences isolated from the Enterococcus facealis genome. AXX12938 to AXX13919 represent these nucleotide sequences which are primary nucleotide sequences. Also known as contigs. The computer-based system can identify fragments of the Enterococcus facealis genome with commercial importance. The products can be used to detect the presence of Enterococcus facealis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus facealis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus facealis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                       A computer readable medium has been developed which has recorded on it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 aatgaatctacacttgttgttgttaccctggaatccccaacctcgcatttcttaaaactttta 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gotottocagtottttccccgttcataaatctcaaagaaccctgcaatccaaatctcta 697
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                                                                                                                                                                                                                  New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 aatgtacgaaagatccaagagggacacctctccatagaccattttggagtgcactctcct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9021 BP; 2967 A; 1582 C; 1878 G; 2581 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62.6; DB 20;
Pred. No. 6.3e-07;
0; Mismatches 399;
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 880-885; 2084pp; English.
                                                                                                                         CA;
                                                                                                                         Kunsch
                                                                       (HUMA-) HUMAN GENOME SCI INC.
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97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity **.. Matches 325; Conservative
                                                                                                                       Dillon PJ,
                                                                                                                                                                     WPI; 1999-045171/04.
06-MAY-1997;
16-MAY-1997;
                                                                                                                       Barash SC,
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Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                  Enterococcus faecalis genome contig SEQ ID NO:81.
     AAX13018 standard; DNA; 15747 BP.
                                                                                         98WO-US08985.
                         (first entry)
                                                            Enterococcus faecalis
                                                                     WO9850555-A2
                         19-MAR-1999
                                                                                         04-MAY-1998;
                                                                               12-NOV-1998.
               AAX13018;
AAX13018
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15

New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection

Kunsch CA;

Barash SC, Dillon PJ,

WPI; 1999-045171/04.

97US-0066009. 97US-0044031. 97US-0046655.

14-NOV-1997; 16-MAY-1997; (HUMA-) HUMAN GENOME SCI INC.

Claim 1; Page 562-570; 2084pp; English.

A computer readable medium has been developed which has recorded on it and solution to the sequences isolated from the Enterococus facalis genome. AAX1938 to AAX19319 represent these nuclectide sequences which are primary nuclectide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococus facalis genome with commercial importance. The products can be used to detect the presence diagnosing Enterococus facalis in samples. They can also be used for diagnosing Enterococus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus facalis, or another related organism, in vivo or in vitro. In particular the products of the Enterococcus facalis in the Enterococcus facalis in the can be used in vaccines to prevent or attenuate an Enterococcal

Séquence 15747 BP; 4949 A; 3274 C; 2618 G; 4899 T; 7 other;

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                                                                                                                    9377 ttaccactttaaataatgtctacgaaggaatctatcgtttagataaagacaacaaaccg 9436
                                                                                                                                                                                                   9437 cgcctgctggtgcagccgaaaaagcgactgtttcagaagacggtttagtttacaaagtta 9496
                                                                                                                                                                                                                                                                                 9497 aattacgtgaagaatcaaaatggtctgatggcaaaccagttactgctgcagattacgtt 9556
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                                                                                                                                                                                                                                                                                                                                                                                                                                  333 tagagoctgotottgoagaagactactctcttcotoggaoggaotcacttatactttta 392
                                                                                                                                                                                                                                           393 a---actgaaatcagctttttggagtaatggcgacccttaacagctgaagactttatag 449
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                                                                                  tcagccttgtcaaacatatctatgagggattagttcaagaaaataatctttcaggaaata 332
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                                                  Gaps
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      Length 15747;
                                              3;
                                              Indels
    Score 60.4; DB 20;
Pred. No. 3.4e-06;
                                          0; Mismatches 201;
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    3.48;
                                      Matches 194; Conservative
Query Match
Best Local Similarity
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